

2 32  
GTT TTA CAC CAT CAC CAA AAC CCA GAA TTT TAT GAT GAG ATT AAA ATA GAG TTG CCC ACT  
val leu his his his gln asn pro glu phe tyr asp glu ile lys ile glu leu pro thr

62 92  
CAG CTG CAT GAA AAG CAC CAC CTG TTG CTC ACA TTC TTC CAT GTC AGC TGT GAC AAC TCA  
gln leu his glu lys his his leu leu leu thr phe phe his val ser cys asp asn ser

122 152  
AGT AAA GGA AGC ACG AAG AAG AGG GAT GTC GTT GAA ACC CAA GTT GGC TAC TCC TGG CTT  
ser lys gly ser thr lys lys arg asp val val glu thr gln val gly tyr ser trp leu

182 212  
CCC CTC CTG AAA GAC GGA AGG GTG GTG ACA AGC GAG CAG CAC ATC CCG GTC TCG GCG AAC  
pro leu leu lys asp gly arg val val thr ser glu gln his ile pro val ser ala asn

242 272  
CTT CCT TCG GGC TAT CTT GGC TAC CAA GAG CTT GGG ATG GGC AGG CAT TAT GGT CCG GAA  
leu pro ser gly tyr leu gly tyr gln glu leu gly met gly arg his tyr gly pro glu

302 332  
ATT AAA TGG GTA GAT GGA GGC AAG CCA CTG CTG AAA ATT TCC ACT CAT CTG GTT TCT ACA  
ile lys trp val asp gly gly lys pro leu leu lys ile ser thr his leu val ser thr

362 392  
GTG TAT ACT CAG GAT CAG CAT TTA CAT AAT TTT TTC CAG TAC TGT CAG AAA ACC GAA TCT  
val tyr thr gln asp gln his leu his asn phe phe gln tyr cys gln lys thr glu ser

422 452  
GGA GCC CAA GCC TTA GGA AAC GAA CTT GTA AAG TAC CTT AAG AGT CTG CAT GCG ATG GAA  
gly ala gln ala leu gly asn glu leu val lys tyr leu lys ser leu his ala met glu

482 512  
GGC CAC GTG ATG ATC GCC TTC TTG CCC ACT ATC CTA AAC CAG CTG TTC CGA GTC CTC ACC  
gly his val met ile ala phe leu pro thr ile leu asn gln leu phe arg val leu thr

542 572  
AGA GCC ACA CAG GAA GAA GTC GCG GTT AAC GTG ACT CGG GTC ATT ATT CAT GTG GTT GCC  
arg ala thr gln glu glu val ala val asn val thr arg val ile ile his val val ala

602 632  
CAG TGC CAT GAG GAA GGA TTG GAG AGC CAC TTG AGG TCA TAT GTT AAG TAC GCG TAT AAG  
gln cys his glu glu gly leu glu ser his leu arg ser tyr val lys tyr ala tyr lys

662 692  
GCT GAG CCA TAT GTT GCC TCT GAA TAC AAG ACA GTG CAT GAA GAA CTG ACC AAA TCC ATG  
ala glu pro tyr val ala ser glu tyr lys thr val his glu glu leu thr lys ser met

FIG. 1

722 ACC ACG ATT CTC AAG CCT TCT GCC GAT TTC CTC ACC AGC AAC AAA CTA CTG AGG TAC TCA  
thr thr ile leu lys pro ser ala asp phe leu thr ser asn lys leu leu arg tyr ser

782 TGG TTT TTC TTT GAT GTA CTG ATC AAA TCT ATG GCT CAG CAT TTG ATA GAG AAC TCC AAA  
trp phe phe phe asp val leu ile lys ser met ala gln his leu ile glu asn ser lys

842 |Cadherin Cleavage| 872 GTT AAG TTG CTG CGA AAC CAG AGA TTT CCT GCA TCC TAT CAT CAT GCA GCG GAA ACC GTT  
val lys leu leu arg asn gln arg phe pro ala ser tyr his his ala ala glu thr val

902 GTA AAT ATG CTG ATG CCA CAC ATC ACT CAG AAG TTT GGA GAT AAT CCA GAG GCA TCT AAG  
val asn met leu met pro his ile thr gln lys phe gly asp asn pro glu ala ser lys

962 AAC GCG AAT CAT AGC CTT GCT GTC TTC ATC AAG AGA TGT TTC ACC TTC ATG GAC AGG GGC  
asn ala asn his ser leu ala val phe ile lys arg cys phe thr phe met asp arg gly

1022 TTT GTC TTC AAG CAG ATC AAC AAC TAC ATT AGC TGT TTT GCT CCT GGA GAC CCA AAG ACC  
phe val phe lys gln ile asn asn tyr ile ser cys phe ala pro gly asp pro lys thr

1082 CTC TTT GAA TAC AAG TTT GAA TTT CTC CGT GTA GTG TGC AAC CAT GAA CAT TAT ATT CCG  
leu phe glu tyr lys phe glu phe leu arg val val cys asn his glu his tyr ile pro

1142 TTG AAC TTA CCA ATG CCA TTT GGA AAA GGC AGG ATT CAA AGA TAC CAA GAC CTC CAG CTT  
leu asn leu pro met pro phe gly lys gly arg ile gln arg tyr gln asp leu gln leu

1202 GAC TAC TCA TTA ACA GAT GAG TTC TGC AGA AAC CAC TTC TTG GTG GGA CTG TTA CTG AGG  
asp tyr ser leu thr asp glu phe cys arg asn his phe leu val gly leu leu leu arg

xxx| 1292 GAG GTG GGG ACA GCC CTC CAG GAG TTC CGG GAG GTC CGT CTG ATC GCC ATC AGT GTG CTC  
glu val gly thr ala leu gln glu phe arg glu val arg leu ile ala ile ser val leu

1322 AAG AAC CTG CTG ATA AAG CAT TCT TTT GAT GAC AGA TAT GCT TCA AGG AGC CAT CAG GCA  
lys asn leu leu ile lys his ser phe asp asp arg tyr ala ser arg ser his gln ala

1382 AGG ATA GCC ACC CTC TAC CTG CCT CTG TTT GGT CTG CTG ATT GAA AAC GTC CAG CGG ATC  
arg ile ala thr leu tyr leu pro leu phe gly leu leu ile glu asn val gln arg ile

1442 AAT GTG AGG GAT GTG TCA CCC TTC CCT GTG AAC GCG GGC ATG ACC GTG AAG GAT GAA TCC  
asn val arg asp val ser pro phe pro val asn ala gly met thr val lys asp glu ser

1472

FIG. 1 (cont.)

1502  
CTG GCT CTA CCA GCT GTG AAT CCG CTG GTG ACG CCG CAG AAG GGA AGC ACC CTG GAC AAC  
leu ala leu pro ala val asn pro leu val thr pro gln lys gly ser thr leu asp asn

1532  
1562  
AGC CTG CAC AAG GAC CTG CTG GGC GCC ATC TCC GGC ATT GCT TCT CCA TAT ACA ACC TCA  
ser leu his lys asp leu leu gly ala ile ser gly ile ala ser pro tyr thr thr ser

1592  
1622  
ACT CCA AAC ATC AAC AGT GTG AGA AAT GCT GAT TCG AGA GGA TCT CTC ATA AGC ACA GAT  
thr pro asn ile asn ser val arg asn ala asp ser arg gly ser leu ile ser thr asp

1652  
1682  
TCG GGT AAC AGC CTT CCA GAA AGG AAT AGT GAG AAG AGC AAT TCC CTG GAT AAG CAC CAA  
ser gly asn ser leu pro glu arg asn ser glu lys ser asn ser leu asp lys his gln

1712  
1742  
CAA AGT AGC ACA TTG GGA AAT TCC GTG GTT CGC TGT GAT AAA CTT GAC CAG TCT GAG ATT  
gln ser ser thr leu gly asn ser val val arg cys asp lys leu asp gln ser glu ile

1772  
1802  
AAG AGC CTA CTG ATG TGT TTC CTC TAC ATC TTA AAG AGC ATG TCT GAT GAT GCT TTG TTT  
lys ser leu leu met cys phe leu tyr ile leu lys ser met ser asp asp ala leu phe

1832  
1862  
ACA TAT TGG AAC AAG GCT TCA ACA TCT GAA CTT ATG GAT TTT TTT ACA ATA TCT GAA GTC  
thr tyr trp asn lys ala ser thr ser glu leu met asp phe phe thr ile ser glu val

1892  
1922  
TGC CTG CAC CAG TTC CAG TAC ATG GGG AAG CGA TAC ATA GCC AGG AAC CAG GAG GGG TTG  
cys leu his gln phe gln tyr met gly lys arg tyr ile ala arg asn gln glu gly leu

1952  
1982  
GGA CCC ATA GTT CAT GAT CGA AAG TCT CAG ACA TTG CCT GTT TCC CGT AAC AGA ACA GGA  
gly pro ile val his asp arg lys ser gln thr leu pro val ser arg asn arg thr gly

2012  
2042  
ATG ATG CAT GCC AGA TTG CAG CAG CTG GGC AGC CTG GAT AAC TCT CTC ACT TTT AAC CAC  
met met his ala arg leu gln gln leu gly ser leu asp asn ser leu thr phe asn his

2072  
2102  
AGC TAT GGC CAC TCG GAC GCA GAT GTT CTG CAC CAG TCA TTA CTT GAA GCC AAC ATT GCT  
ser tyr gly his ser asp ala asp val leu his gln ser leu leu glu ala asn ile ala

2132  
2162  
ACT GAG GTT TGC CTG ACA GCT CTG GAC ACG CTT TCT CTA TTT ACA TTG GCG TTT AAG AAC  
thr glu val cys leu thr ala leu asp thr leu ser leu phe thr leu ala phe lys asn

2192  
2222  
CAG CTC CTG GCC GAC CAT GGA CAT AAT CCT CTC ATG AAA AAA GTT TTT GAT GTC TAC CTG  
gln leu leu ala asp his gly his asn pro leu met lys lys val phe asp val tyr leu

2252  
2282  
TGT TTT CTT CAA AAA CAT CAG TCT GAA ACG GCT TTA AAA AAT GTC TTC ACT GCC TTA AGG

2312

Fig. 1 (cont.)





arg leu ile lys glu asp gln leu glu tyr gln glu glu met lys ala asn tyr arg glu

3902 xxx Coiled-Coil 2 xxxxxxxxxxxxxxxx 3932 xxxxx|

ATG GCG AAG GAG CTT TCT GAA ATC ATG CAT GAG CAG ATC TGC CCC CTG GAG GAG AAG ACG  
met ala lys glu leu ser glu ile met his glu gln ile cys pro leu glu glu lys thr

3962

3992

AGC GTC TTA CCG AAT TCC CTT CAC ATC TTC AAC GCC ATC AGT GGG ACT CCA ACA AGC ACA  
ser val leu pro asn ser leu his ile phe asn ala ile ser gly thr pro thr ser thr

4022

|xxxxx PBM xxxxx|

ATG GTT CAC GGG ATG ACC AGC TCG TCT TCG GTC GTG TGA TTA CAT CTC ATG GCC CGT GTG  
met val his gly met thr ser ser ser ser val val STP

4082

4112

TGG GGA CTT GCT TTG TCA TTT GCA AAC TCA GGA TGC TTT CCA AAG CCA ATC ACT GGG GAG

4142

4172

ACC GAG CAC AGG GAG GAC CAA GGG GAA GGG GAG AGA AAG GAA ATA AAG AAC AAC GTT ATT

4202

4232

TCT TAA CAG ACT TTC TAT AGG AGT TGT AAG AAG GTG CAC ATA TTT TTT TAA ATC TCA CTG

4262

4292

GCA ATA TTC AAA GTT TTC ATT GTG TCT TAA CAA AGG TGT GGT AGA CAC TCT TGA GCT GGA

4322

4352

CTT AGA TTT TAT TCT TCC TTG CAG AGT AGT GTT AGA ATA GAT GGC CTA CAG AAA AAA AAG

4382

4412

GTT CTG GGA TCT ACA TGG CAG GGA GGG CTG CAC TGA CAT TGA TGC CTG GGG GAC CTT TTG

4442

4472

CCT CGA CTC GTG CCG GAA ATC TGA TCG TAA TCA GGG TAC AGA ACT TAC TAG TTT TGT CTA

4502

4532

GGA GTA TGT TGT ATG ACT AGG ATT TGT GCT ATT ATC TCA TTC AAC AAC ATA GAG CAA GAA

4562

4592

TAG TGA GCT AAC TGA GCT AGA CAC TCA ATT AAT CCG CTA CTG GCT TCA AGT CAG AAC TTT

4622

4652

GTC ATT AAT CAT CGA CTC CGG GAC GGT CAT ATA TGT ATT ACA TTT CTA CAT TTT TAA TAC

4682

4712

TCA CAT GGG CTT ATG CAT TAA GTT TAA TTG TGA TAA ATT TGT GCT GGT CCA GTA TAT GCA

4742

4772

ATA CAC TTT AAT GGT TTA TTC TTG TCA TAA AAA TGT GCA ATA TGG AGA TGT ATA CAA GTC

4802

TTT ACT

Fig. 1 (cont.)

(Nucleotide position for insertions and deletion are found above the Human (h) CLASP-2A line diagram. Numbers are referenced based on hCLASP-2A nucleotide sequence from Figure 1.)

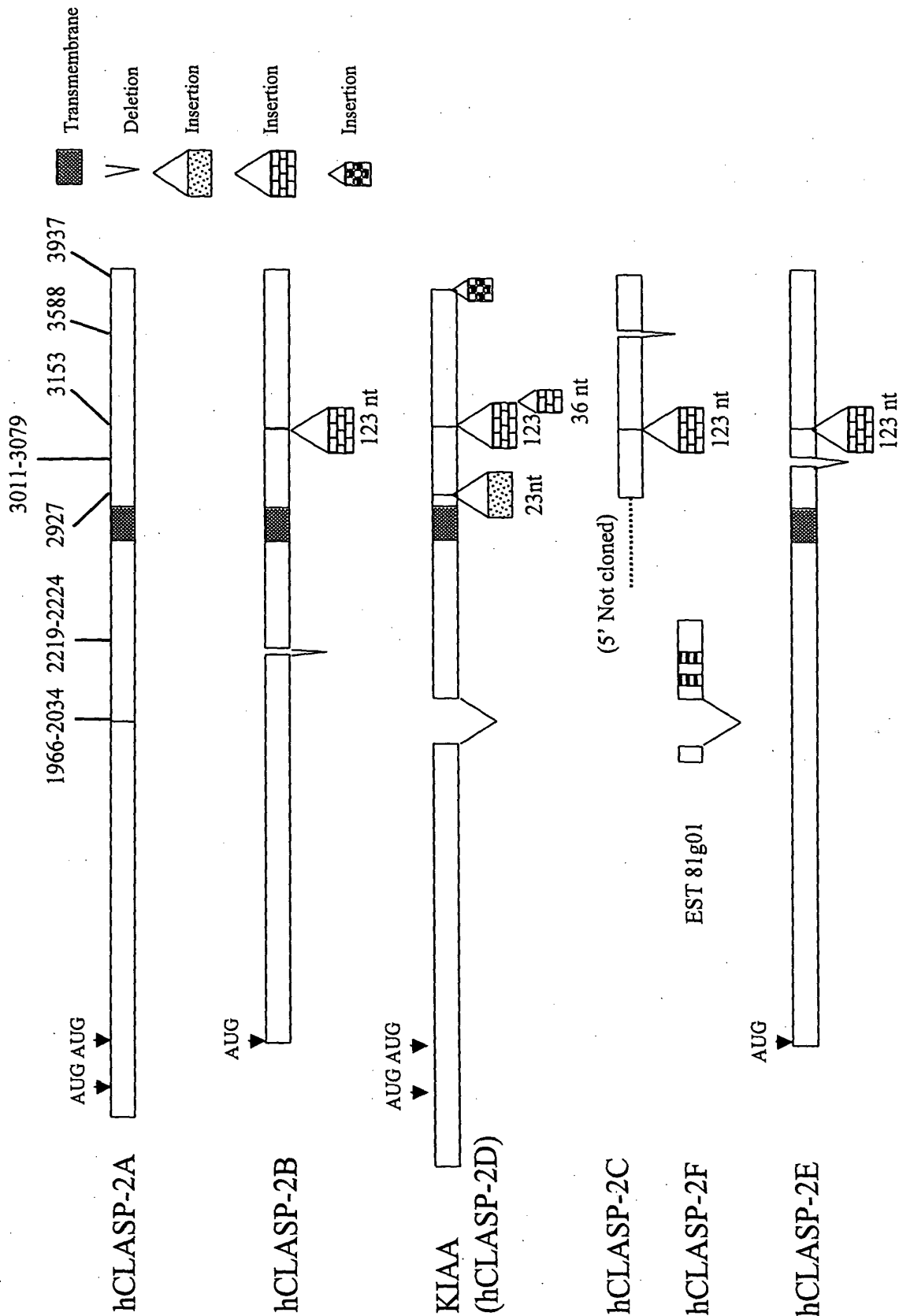


FIG. 2A

2 32  
GTT TTA CAC CAT CAC CAA AAC CCA GAA TTT TAT GAT GAG ATT AAA ATA GAG TTG CCC ACT  
val leu his his his gln asn pro glu phe tyr asp glu ile lys ile glu leu pro thr

62 72  
CAG CTG CAT GAA AAG CAC CAC CTG TTG CTC ACA TTC TTC CAT GTC AGC TGT GAC AAC TCA  
gln leu his glu lys his his leu leu leu thr phe phe his val ser cys asp asn ser

122 152  
AGT AAA GGA AGC ACG AAG AAG AGG GAT GTC GTT GAA ACC CAA GTT GGC TAC TCC TGG CTT  
ser lys gly ser thr lys lys arg asp val val glu thr gln val gly tyr ser trp leu

182 212  
CCC CTC CTG AAA GAC GGA AGG GTG GTG ACA AGC GAG CAG CAC ATC CCG GTC TCG GCG AAC  
pro leu leu lys asp gly arg val val thr ser glu gln his ile pro val ser ala asn

242 272  
CTT CCT TCG GGC TAT CTT GGC TAC CAA GAG CTT GGG ATG GGC AGG CAT TAT GGT CCG GAA  
leu pro ser gly tyr leu gly tyr gln glu leu gly met gly arg his tyr gly pro glu

302 332  
ATT AAA TGG GTA GAT GGA GGC AAG CCA CTG CTG AAA ATT TCC ACT CAT CTG GTT TCT ACA  
ile lys trp val asp gly gly lys pro leu leu lys ile ser thr his leu val ser thr

362 392  
GTG TAT ACT CAG GAT CAG CAT TTA CAT AAT TTT TTC CAG TAC TGT CAG AAA ACC GAA TCT  
val tyr thr gln asp gln his leu his asn phe phe gln tyr cys gln lys thr glu ser

422 452  
GGA GCC CAA GCC TTA GGA AAC GAA CTT GTA AAG TAC CTT AAG AGT CTG CAT GCG ATG GAA  
gly ala gln ala leu gly asn glu leu val lys tyr leu lys ser leu his ala met glu

482 512  
GGC CAC GTG ATG ATC GCC TTC TTG CCC ACT ATC CTA AAC CAG CTG TTC CGA GTC CTC ACC  
gly his val met ile ala phe leu pro thr ile leu asn gln leu phe arg val leu thr

542 572  
AGA GCC ACA CAG GAA GAA GTC GCG GTT AAC GTG ACT CGG GTC ATT ATT CAT GTG GTT GCC  
arg ala thr gln glu glu val ala val asn val thr arg val ile ile his val val ala

602 632  
CAG TGC CAT GAG GAA GGA TTG GAG AGC CAC TTG AGG TCA TAT GTT AAG TAC GCG TAT AAG  
gln cys his glu glu gly leu glu ser his leu arg ser tyr val lys tyr ala tyr lys

662 692  
GCT GAG CCA TAT GTT GCC TCT GAA TAC AAG ACA GTG CAT GAA GAA CTG ACC AAA TCC ATG  
ala glu pro tyr val ala ser glu tyr lys thr val his glu glu leu thr lys ser met

FIG. 2B



722 752  
ACC ACG ATT CTC AAG CCT TCT GCC GAT TTC CTC ACC AGC AAC AAA CTA CTG AGG TAC TCA  
thr thr ile leu lys pro ser ala asp phe leu thr ser asn lys leu leu arg tyr ser

782 812  
TGG TTT TTC TTT GAT GTA CTG ATC AAA TCT ATG GCT CAG CAT TTG ATA GAG AAC TCC AAA  
trp phe phe phe asp val leu ile lys ser met ala gln his leu ile glu asn ser lys

842 |Cadherin Cleavage| 872  
GTT AAG TTG CTG CGA AAC CAG AGA TTT CCT GCA TCC TAT CAT CAT GCA GCG GAA ACC GTT  
val lys leu leu arg asn gln arg phe pro ala ser tyr his his ala ala glu thr val

902 932  
GTA AAT ATG CTG ATG CCA CAC ATC ACT CAG AAG TTT GGA GAT AAT CCA GAG GCA TCT AAG  
val asn met leu met pro his ile thr gln lys phe gly asp asn pro glu ala ser lys

962 992  
AAC GCG AAT CAT AGC CTT GCT GTC TTC ATC AAG AGA TGT TTC ACC TTC ATG GAC AGG GGC  
asn ala asn his ser leu ala val phe ile lys arg cys phe thr phe met asp arg gly

1022 1052  
TTT GTC TTC AAG CAG ATC AAC AAC TAC ATT AGC TGT TTT GCT CCT GGA GAC CCA AAG ACC  
phe val phe lys gln ile asn asn tyr ile ser cys phe ala pro gly asp pro lys thr

1082 1112  
CTC TTT GAA TAC AAG TTT GAA TTT CTC CGT GTA GTG TGC AAC CAT GAA CAT TAT ATT CCG  
leu phe glu tyr lys phe glu phe leu arg val val cys asn his glu his tyr ile pro

1142 1172  
TTG AAC TTA CCA ATG CCA TTT GGA AAA GGC AGG ATT CAA AGA TAC CAA GAC CTC CAG CTT  
leu asn leu pro met pro phe gly lys gly arg ile gln arg tyr gln asp leu gln leu

1202 1232 |Cadherin EC  
GAC TAC TCA TTA ACA GAT GAG TTC TGC AGA AAC CAC TTC TTG GTG GGA CTG TTA CTG AGG  
asp tyr ser leu thr asp glu phe cys arg asn his phe leu val gly leu leu leu arg

xxx! 1292  
GAG GTG GGG ACA GCC CTC CAG GAG TTC CGG GAG GTC CGT CTG ATC GCC ATC AGT GTG CTC  
glu val gly thr ala leu gln glu phe arg glu val arg leu ile ala ile ser val leu

1322 1352  
AAG AAC CTG CTG ATA AAG CAT TCT TTT GAT GAC AGA TAT GCT TCA AGG AGC CAT CAG GCA  
lys asn leu leu ile lys his ser phe asp asp arg tyr ala ser arg ser his gln ala

1382 1412  
AGG ATA GCC ACC CTC TAC CTG CCT CTG TTT GGT CTG CTG ATT GAA AAC GTC CAG CGG ATC  
arg ile ala thr leu tyr leu pro leu phe gly leu leu ile glu asn val gln arg ile

1442 1472  
AAT GTG AGG GAT GTG TCA CCC TTC CCT GTG AAC GCG GGC ATG ACC GTG AAG GAT GAA TCC  
asn val arg asp val ser pro phe pro val asn ala gly met thr val lys asp glu ser

Fig. 2B (cont.)

1502 1532  
 CTG GCT CTA CCA GCT GTG AAT CCG CTG GTG ACG CCG CAG AAG GGA AGC ACC CTG GAC AAC  
 leu ala leu pro ala val asn pro leu val thr pro gln lys gly ser thr leu asp asn

1562 1592  
 AGC CTG CAC AAG GAC CTG CTG GGC GCC ATC TCC GGC ATT GCT TCT CCA TAT ACA ACC TCA  
 ser leu his lys asp leu leu gly ala ile ser gly ile ala ser pro tyr thr thr ser

1622 1652  
 ACT CCA AAC ATC AAC AGT GTG AGA AAT GCT GAT TCG AGA GGA TCT CTC ATA AGC ACA GAT  
 thr pro asn ile asn ser val arg asn ala asp ser arg gly ser leu ile ser thr asp

1682 1712  
 TCG GGT AAC AGC CTT CCA GAA AGG AAT AGT GAG AAG AGC AAT TCC CTG GAT AAG CAC CAA  
 ser gly asn ser leu pro glu arg asn ser glu lys ser asn ser leu asp lys his gln

1742 1772  
 CAA AGT AGC ACA TTG GGA AAT TCC GTG GTT CGC TGT GAT AAA CTT GAC CAG TCT GAG ATT  
 gln ser ser thr leu gly asn ser val val arg cys asp lys leu asp gln ser glu ile

1802 1832  
 AAG AGC CTA CTG ATG TGT TTC CTC TAC ATC TTA AAG AGC ATG TCT GAT GAT GCT TTG TTT  
 lys ser leu leu met cys phe leu tyr ile leu lys ser met ser asp asp ala leu phe

1862 1892  
 ACA TAT TGG AAC AAG GCT TCA ACA TCT GAA CTT ATG GAT TTT TTT ACA ATA TCT GAA GTC  
 thr tyr trp asn lys ala ser thr ser glu leu met asp phe phe thr ile ser glu val

1922 1952 |xxxxxxxxxxxxxxxxxxxxxx  
 TGC CTG CAC CAG TTC CAG TAC ATG GGG AAG CGA TAC ATA GCC AGG AAC CAG GAG GGG TTG  
 cys leu his gln phe gln tyr met gly lys arg tyr ile ala arg asn gln glu gly leu

1982 xxxxxxxxxx deleted in CLASP-2D(KIAA1058) xxxxxxxxxxxxxxxxxxxxxxxx  
 GGA CCC ATA GTT CAT GAT CGA AAG TCT CAG ACA TTG CCT GTT TCC CGT AAC AGA ACA GGA  
 gly pro ile val his asp arg lys ser gln thr leu pro val ser arg asn arg thr gly

2042 2072  
 ATG ATG CAT GCC AGA TTG CAG CAG CTG GGC AGC CTG GAT AAC TCT CTC ACT TTT AAC CAC  
 met met his ala arg leu gln gln leu gly ser leu asp asn ser leu thr phe asn his

2102 2132  
 AGC TAT GGC CAC TCG GAC GCA GAT GTT CTG CAC CAG TCA TTA CTT GAA GCC AAC ATT GCT  
 ser tyr gly his ser asp ala asp val leu his gln ser leu leu glu ala asn ile ala

2162 2192 Deleted  
 |xxx  
 ACT GAG GTT TGC CTG ACA GCT CTG GAC ACG CTT TCT CTA TTT ACA TTG GCG TTT AAG AAC  
 thr glu val cys leu thr ala leu asp thr leu ser leu phe thr leu ala phe lys asn

in HC2B  
 xxxl 2252  
 CAG CTC CTG GCC GAC CAT GGA CAT AAT CCT CTC ATG AAA AAA GTT TTT GAT GTC TAC CTG  
 gln leu leu ala asp his gly his asn pro leu met lys lys val phe asp val tyr leu

Fig. 2B (cont.)

2282 2312  
TGT TTT CTT CAA AAA CAT CAG TCT GAA ACG GCT TTA AAA AAT GTC TTC ACT GCC TTA AGG  
cys phe leu gln lys his gln ser glu thr ala leu lys asn val phe thr ala leu arg

2342 2372  
TCC TTA ATT TAT AAG TTT CCC TCA ACA TTC TAT GAA GGG AGA GCG GAC ATG TGT GCG GCT  
ser leu ile tyr lys phe pro ser thr phe tyr glu gly arg ala asp met cys ala ala

2402 2432  
CTG TGT TAC GAG ATT CTC AAG TGC TGT AAC TCC AAG CTG AGC TCC ATC AGG ACG GAG GCC  
leu cys tyr glu ile leu lys cys cys asn ser lys leu ser ser ile arg thr glu ala

2462 2492  
TCC CAG CTG CTC TAC TTC CTG ATG AGG AAC AAC TTT GAT TAC ACT GGA AAG AAG TCC TTT  
ser gln leu leu tyr phe leu met arg asn asn phe asp tyr thr gly lys lys ser phe

2522 2552  
GTC CGG ACA CAT TTG CAA GTC ATC ATA TCT GTC AGC CAG CTG ATA GCA GAC GTT GTT GGC  
val arg thr his leu gln val ile ile ser val ser gln leu ile ala asp val val gly

2582 2612  
ATT GGG GAA ACC AGA TTC CAG CAG TCC CTG TCC ATC ATC AAC AAC TGT GCC AAC AGT GAC  
ile gly glu thr arg phe gln gln ser leu ser ile ile asn asn cys ala asn ser asp

2642 2672  
GGG CTT ATT AAG CAC ACC AGC TTC TCC TCT GAT GTG AAG GAC TTA ACC AAA AGG ATA CGC  
arg leu ile lys his thr ser phe ser ser asp val lys asp leu thr lys arg ile arg

2702 2732  
ACG GTG CTA ATG GCC ACC GCC CAG ATG AAG GAG CAT GAG AAC GAC CCA GAG ATG CTG GTG  
thr val leu met ala thr ala gln met lys glu his glu asn asp pro glu met leu val

2762 2792  
GAC CTC CAG TAC AGC CTG GCC AAA TCC TAT GCC AGC ACG CCC GAG CTC AGG AAG ACG TGG  
asp leu gln tyr ser leu ala lys ser tyr ala ser thr pro glu leu arg lys thr trp

2822 2852 lxxxxxxxxxxxxxxxx Predicted  
CTC GAC AGC ATG GCC AGG ATC CAT GTC AAA AAT GGC GAT CTC TCA GAG GCA GCA ATG TGC  
leu asp ser met ala arg ile his val lys asn gly asp leu ser glu ala ala met cys

[[Additional and differential exon usage found at position 2927 consisting  
of 69 nucleotides. This entire sequence is found in Human CLASP-2D  
(KIAA1058) and not other isoforms of CLASP-2. It has a sequence of:  
AAGCAGTCCAGTGGGAGCCGCCCTTCTCCCCACAGCCATAGCGCCTGCCTGAGGAGGAGCCGGGGAG]]

Transmembrane Domain xxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxx|

TAT GTC CAC GTA ACA GCC CTA GTG GCA GAA TAT CTC ACA CGG AAA GGC GTG TTT AGA CAA  
tyr val his val thr ala leu val ala glu tyr leu thr arg lys gly val phe arg gln

2942 2972  
GGA TGC ACC GCC TTC AGG GTC ATT ACC CCA AAC ATC GAC GAG GAG GCC TCC ATG ATG GAA  
gly cys thr ala phe arg val ile thr pro asn ile asp glu glu ala ser met met glu

Fig. 2B (cont.)

3002 |xxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxx Sequence deleted in CLASP-2E xxxxx  
 GAC GTG GGG ATG CAG GAT GTC CAT TTC AAC GAG GAT GTG CTG ATG GAG CTC CTT GAG CAG  
 asp val gly met gln asp val his phe asn glu asp val leu met glu leu leu glu gln

3062 xxxxxxxxxxxxxxxxxxxxxxxx| 3092  
 TGC GCA GAT GGA CTC TGG AAA GCC GAG CGC TAC GAG CTC ATC GCC GAC ATC TAC AAA CTT  
 cys ala asp gly leu trp lys ala glu arg tyr glu leu ile ala asp ile tyr lys leu

[Additional and differential exon usage found at position 3153. The entire sequence below is found in Human CLASP-2D. Underlined sequence is found in Human CLASP-2B, 2C and 2E.

TGAGAGGCTGGCCCATCTGTATGACACGCTGCACCGGGCCTACAGCAAAGTGACCGAGGTCAT  
 GCACTCGGGCCGCAGGCTTCTGGGGACCTACTTCCGGGTAGCCTTCTTCGGGCAGGCAGCGCAATACCAAGTTT  
 ACAGACAGTGAACAGATGTGGAGGGATT]



3122 3155  
 ATC ATC CCC ATT TAT GAG AAG CGG AGG GAT TTC TTT GAA GAT GAA GAT GGA AAG GAG TAT  
 ile ile pro ile tyr glu lys arg arg asp phe phe glu asp glu asp gly lys glu tyr

3182 3212  
 ATT TAC AAG GAA CCC AAA CTC ACA CCG CTG TCG GAA ATT TCT CAG AGA CTC CTT AAA CTG  
 ile tyr lys glu pro lys leu thr pro leu ser glu ile ser gln arg leu leu lys leu

3242 3272  
 TAC TCG GAT AAA TTT GGT TCT GAA AAT GTC AAA ATG ATA CAG GAT TCT GGC AAG GTC AAC  
 tyr ser asp lys phe gly ser glu asn val lys met ile gln asp ser gly lys val asn

3302 3332  
 CCT AAG GAT CTG GAT TCT AAG TAT GCA TAC ATC CAG GTG ACT CAC GTC ATC CCC TTC TTT  
 pro lys asp leu asp ser lys tyr ala tyr ile gln val thr his val ile pro phe phe

3362 3392  
 GAC GAA AAA GAG TTG CAA GAA AGG AAA ACA GAG TTT GAG AGA TCC CAC AAC ATC CGC CGC  
 asp glu lys glu leu gln glu arg lys thr glu phe glu arg ser his asn ile arg arg

3422 3452  
 TTC ATG TTT GAG ATG CCA TTT ACG CAG ACC GGG AAG AGG CAG GGC GGG GTG GAA GAG CAG  
 phe met phe glu met pro phe thr gln thr gly lys arg gln gly gly val glu glu gln

3482 3512  
 TGC AAA CGG CGC ACC ATC CTG ACA GCC ATA CAC TGC TTC CCT TAT GTG AAG AAG CGC ATC  
 cys lys arg arg thr ile leu thr ala ile his cys phe pro tyr val lys lys arg ile

Two nucleotide deletion (nts 3586 and 3587) found in Human CLASP-2C



3542 3572 |xxx|  
 CCT GTC ATG TAC CAG CAC CAC ACT GAC CTG AAC CCC ATC GAG GTG GCC ATT GAC GAG ATG  
 pro val met tyr gln his his thr asp leu asn pro ile glu val ala ile asp glu met

Fig. 2B (cont.)

3602 3632  
AGT AAG AAG GTG GCG GAG CTC CGG CAG CTG TGC TCC TCG GCC GAG GTG GAC ATG ATC AAA  
ser lys lys val ala glu leu arg gln leu cys ser ser ala glu val asp met ile lys

3662 3692  
CTG CAG CTC AAA CTC CAG GGC AGC GTG AGT GTT CAG GTC AAT GCT GGC CCA CTA GCA TAT  
leu gln leu lys leu gln gly ser val ser val gln val asn ala gly pro leu ala tyr

3722 3752  
GCG CGA GCT TTC TTA GAT GAT ACA AAC ACA AAG CGA TAT CCT GAC AAT AAA GTG AAG CTG  
ala arg ala phe leu asp asp thr asn thr lys arg tyr pro asp asn lys val lys leu

3782 3812  
CTT AAG GAA GTT TTC AGG CAA TTT GTG GAA GCT TGC GGT CAA GCC TTA GCG GTA AAC GAA  
leu lys glu val phe arg gln phe val glu ala cys gly gln ala leu ala val asn glu

3842 3872  
CGT CTG ATT AAA GAA GAC CAG CTC GAG TAT CAG GAA GAA ATG AAA GCC AAC TAC AGG GAA  
arg leu ile lys glu asp gln leu glu tyr gln glu glu met lys ala asn tyr arg glu

Insertion of 8 nucleotides found only in Human CLASP-2D with sequence: CTGGGATG

3902 3932  
ATG GCG AAG GAG CTT TCT GAA ATC ATG CAT GAG CAG ATC TGC CCC CTG GAG GAG AAG ACG  
met ala lys glu leu ser glu ile met his glu gln ile cys pro leu glu glu lys thr

3962 3992  
AGC GTC TTA CCG AAT TCC CTT CAC ATC TTC AAC GCC ATC AGT GGG ACT CCA ACA AGC ACA  
ser val leu pro asn ser leu his ile phe asn ala ile ser gly thr pro thr ser thr

4022 (xxxx PBM xxxx)  
ATG GTT CAC GGG ATG ACC AGC TCG TCT TCG GTC GTG TGA TTA CAT CTC ATG GCC CGT GTG  
met val his gly met thr ser ser ser ser val val STP

4082 4112  
TGG GGA CTT GCT TTG TCA TTT GCA AAC TCA GGA TGC TTT CCA AAG CCA ATC ACT GGG GAG

4142 4172  
ACC GAG CAC AGG GAG GAC CAA GGG GAA GGG GAG AGA AAG GAA ATA AAG AAC AAC GTT ATT

4202 4232  
TCT TAA CAG ACT TTC TAT AGG AGT TGT AAG AAG GTG CAC ATA TTT TTT TAA ATC TCA CTG

4262 4292  
GCA ATA TTC AAA GTT TTC ATT GTG TCT TAA CAA AGG TGT GGT AGA CAC TCT TGA GCT GGA

4322 4352  
CTT AGA TTT TAT TCT TCC TTG CAG AGT AGT GTT AGA ATA GAT GGC CTA CAG AAA AAA AAG

4382 4412  
GTT CTG GGA TCT ACA TGG CAG GGA GGG CTG CAC TGA CAT TGA TGC CTG GGG GAC CTT TTG

4442 4472

Fig. 2B (cont.)

CCT CGA CTC GTG CCG GAA ATC TGA TCG TAA TCA GGG TAC AGA ACT TAC TAG TTT TGT CTA

4502

4532

GGA GTA TGT TGT ATG ACT AGG ATT TGT GCT ATT ATC TCA TTC AAC AAC ATA GAG CAA GAA

4562

4592

TAG TGA GCT AAC TGA GCT AGA CAC TCA ATT AAT CCG CTA CTG GCT TCA AGT CAG AAC TTT

4622

4652

GTC ATT AAT CAT CGA CTC CGG GAC GGT CAT ATA TGT ATT ACA TTT CTA CAT TTT TAA TAC

4682

4712

TCA CAT GGG CTT ATG CAT TAA GTT TAA TTG TGA TAA ATT TGT GCT GGT CCA GTA TAT GCA

4742

4772

ATA CAC TTT AAT GGT TTA TTC TTG TCA TAA AAA TGT GCA ATA TGG AGA TGT ATA CAA GTC

4802

TTT ACT

09687837 101300

Fig. 2B (cont.)

|               |                                                              |
|---------------|--------------------------------------------------------------|
| HC2A          | -----                                                        |
| HC2-80        | -----                                                        |
| HC2B          | -----                                                        |
| HC2C          | -----                                                        |
| HC2D-KIAA1058 | GCATCTGGAAATCTTGACAAAAATGCCAGATTTTCTGCCATCTACAGGCAAGACAGCAAT |
| HC2E          | -----                                                        |
| HC2F          | -----                                                        |

|               |                                                               |
|---------------|---------------------------------------------------------------|
| HC2A          | -----                                                         |
| HC2-80        | -----                                                         |
| HC2B          | -----                                                         |
| HC2C          | -----                                                         |
| HC2D-KIAA1058 | AAGCTATCCAATGATGACATGCTCAAGTTACTTGACAGACTTTCGGAAACCTGAGAAGATG |
| HC2E          | -----                                                         |
| HC2F          | -----                                                         |

|               |                                                              |
|---------------|--------------------------------------------------------------|
| HC2A          | -----                                                        |
| HC2-80        | -----                                                        |
| HC2B          | -----                                                        |
| HC2C          | -----                                                        |
| HC2D-KIAA1058 | GCTAAGCTCCCAGTGATTTTAGGCAATCTAGACATTACAATTGATAATGTTTCCTCAGAC |
| HC2E          | -----                                                        |
| HC2F          | -----                                                        |

|               |                                                             |
|---------------|-------------------------------------------------------------|
| HC2A          | -----                                                       |
| HC2-80        | -----                                                       |
| HC2B          | -----                                                       |
| HC2C          | -----                                                       |
| HC2D-KIAA1058 | TTCCCTAATTATGTTAATTCATCATAATTCCCACAAAACAATTTGAAACCTGCAGTAAA |
| HC2E          | -----                                                       |
| HC2F          | -----                                                       |

|               |                                                              |
|---------------|--------------------------------------------------------------|
| HC2A          | -----                                                        |
| HC2-80        | -----                                                        |
| HC2B          | -----                                                        |
| HC2C          | -----                                                        |
| HC2D-KIAA1058 | ACTCCCATCACGTTTGAAGTGGAGGAATTTGTGCCCTGCATACCAAAACACACTCAGCCT |
| HC2E          | -----                                                        |
| HC2F          | -----                                                        |

FIG. 3A

|               |                                                              |
|---------------|--------------------------------------------------------------|
| HC2A          | -----                                                        |
| HC2-80        | -----                                                        |
| HC2B          | -----                                                        |
| HC2C          | -----                                                        |
| HC2D-KIAA1058 | TACACCATCTACACCAATCACCTTTACGTTTATCCTAAGTACTTGAAATACGACAGTCAG |
| HC2E          | -----                                                        |
| HC2F          | -----                                                        |

|               |                                                              |
|---------------|--------------------------------------------------------------|
| HC2A          | -----                                                        |
| HC2-80        | -----                                                        |
| HC2B          | -----                                                        |
| HC2C          | -----                                                        |
| HC2D-KIAA1058 | AAGTCTTTTGCCAAGGCTAGAAATATTGCGATTTGCATTGAATTCAAAGATTCAGATGAG |
| HC2E          | -----                                                        |
| HC2F          | -----                                                        |

|               |                                                                |
|---------------|----------------------------------------------------------------|
| HC2A          | -----                                                          |
| HC2-80        | -----                                                          |
| HC2B          | -----                                                          |
| HC2C          | -----                                                          |
| HC2D-KIAA1058 | GAAGACTCTCAGCCCCCTTAAGTGCATTTATGGCAGACCTGGTGGGCCAGTTTTTCACAAGA |
| HC2E          | -----                                                          |
| HC2F          | -----                                                          |

|               |                                                              |
|---------------|--------------------------------------------------------------|
| HC2A          | -----AGTTTTACACCATCACCAAAACCCAGAATTTTATGATGAGATTAAA          |
| HC2-80        | -----                                                        |
| HC2B          | -----                                                        |
| HC2C          | -----                                                        |
| HC2D-KIAA1058 | AGCGCCTTTGCTGCAGTTTTACACCATCACCAAAACCCAGAATTTTATGATGAGATTAAA |
| HC2E          | -----                                                        |
| HC2F          | -----                                                        |

|               |                                                             |
|---------------|-------------------------------------------------------------|
| HC2A          | ATAGAGTTGCCCACTCAGCTGCATGAAAAGCACCACTGTTGCTCACATTCTTCCATGTC |
| HC2-80        | -----                                                       |
| HC2B          | -----                                                       |
| HC2C          | -----                                                       |
| HC2D-KIAA1058 | ATAGAGTTGCCCACTCAGCTGCATGAAAAGCACCACTGTTGCTCACATTCTTCCATGTC |
| HC2E          | -----                                                       |
| HC2F          | -----                                                       |

|               |                                                               |
|---------------|---------------------------------------------------------------|
| HC2A          | AGCTGTGACAACCTCAAGTAAAGGAAGCACGAAGAAGAGGGATGTCGTTGAAACCCAAGTT |
| HC2-80        | -----                                                         |
| HC2B          | -----                                                         |
| HC2C          | -----                                                         |
| HC2D-KIAA1058 | AGCTGTGACAACCTCAAGTAAAGGAAGCACGAAGAAGAGGGATGTCGTTGAAACCCAAGTT |
| HC2E          | -----                                                         |
| HC2F          | -----                                                         |

FIG. 3A (cont.)



|               |                                                              |
|---------------|--------------------------------------------------------------|
| HC2A          | GGCTACTCCTGGCTTCCCCTCCTGAAAGACGGAAGGGTGGTGACAAGCGAGCAGCACATC |
| HC2-80        | -----                                                        |
| HC2B          | -----                                                        |
| HC2C          | -----                                                        |
| HC2D-KIAA1058 | GGCTACTCCTGGCTTCCCCTCCTGAAAGACGGAAGGGTGGTGACAAGCGAGCAGCACATC |
| HC2E          | -----                                                        |
| HC2F          | -----                                                        |

|               |                                                              |
|---------------|--------------------------------------------------------------|
| HC2A          | CCGGTCTCGGCGAACCTTCCTTCGGGCTATCTTGGCTACCAAGAGCTTGGGATGGGCAGG |
| HC2-80        | -----                                                        |
| HC2B          | -----                                                        |
| HC2C          | -----                                                        |
| HC2D-KIAA1058 | CCGGTCTCGGCGAACCTTCCTTCGGGCTATCTTGGCTACCAGGAGCTTGGGATGGGCAGG |
| HC2E          | -----                                                        |
| HC2F          | -----                                                        |

|               |                                                              |
|---------------|--------------------------------------------------------------|
| HC2A          | CATTATGGTCCGGAAATTAAATGGGTAGATGGAGGCAAGCCACTGCTGAAAATTTCCACT |
| HC2-80        | -----                                                        |
| HC2B          | -----                                                        |
| HC2C          | -----                                                        |
| HC2D-KIAA1058 | CATTATGGTCCGGAAATTAAATGGGTAGATGGAGGCAAGCCACTGCTGAAAATTTCCACT |
| HC2E          | -----                                                        |
| HC2F          | -----                                                        |

|               |                                                             |
|---------------|-------------------------------------------------------------|
| HC2A          | CATCTGGTTTCTACAGTGTATACTCAGGATCAGCATTACATAATTTTTTCCAGTACTGT |
| HC2-80        | -----                                                       |
| HC2B          | -----                                                       |
| HC2C          | -----                                                       |
| HC2D-KIAA1058 | CATCTGGTTTCTACAGTGTATACTCAGGATCAGCATTACATAATTTTTTCCAGTACTGT |
| HC2E          | -----                                                       |
| HC2F          | -----                                                       |

|               |                                                              |
|---------------|--------------------------------------------------------------|
| HC2A          | CAGAAAACCGAATCTGGAGCCCCAAGCCTTAGGAAACGAACTTGTAAGTACCTTAAGAGT |
| HC2-80        | -----                                                        |
| HC2B          | -----                                                        |
| HC2C          | -----                                                        |
| HC2D-KIAA1058 | CAGAAAACCGAATCTGGAGCCCCAAGCCTTAGGAAACGAACTTGTAAGTACCTTAAGAGT |
| HC2E          | -----                                                        |
| HC2F          | -----                                                        |

|               |                                                              |
|---------------|--------------------------------------------------------------|
| HC2A          | CTGCATGCGATGGAAGGCCACGTGATGATCGCCTTCTTGCCCACTATCCTAAACCAGCTG |
| HC2-80        | -----                                                        |
| HC2B          | -----GCGATGGAAGGCCACGTGATGATCGCCTTCTTGCCCACTATCCTAAACCAGCTG  |
| HC2C          | -----                                                        |
| HC2D-KIAA1058 | CTGCATGCGATGGAAGGCCACGTGATGATCGCCTTCTTGCCCACTATCCTAAACCAGCTG |
| HC2E          | -----GCGATGGAAGGCCACGTGATGATCGCCTTCTTGCCCACTATCCTAAACCAGCTG  |
| HC2F          | -----                                                        |

|               |                                                              |
|---------------|--------------------------------------------------------------|
| HC2A          | TTCCGAGTCCTCACCAGAGCCACACAGGAAGAAGTCGCGGTAAACGTGACTCGGGTCATT |
| HC2-80        | -----                                                        |
| HC2B          | TTCCGAGTCCTCACCAGAGCCACACAGGAAGAAGTCGCGGTAAACGTGACTCGGGTCATT |
| HC2C          | -----                                                        |
| HC2D-KIAA1058 | TTCCGAGTCCTCACCAGAGCCACACAGGAAGAAGTCGCGGTAAACGTGACTCGGGTCATT |
| HC2E          | TTCCGAGTCCTCACCAGAGCCACACAGGAAGAAGTCGCGGTAAACGTGACTCGGGTCATT |
| HC2F          | -----                                                        |
|               |                                                              |
| HC2A          | ATTCATGTGGTTGCCAGTGCCATGAGGAAGGATTGGAGAGCCACTTGAGGTCATATGTT  |
| HC2-80        | -----                                                        |
| HC2B          | ATTCATGTGGTTGCCAGTGCCATGAGGAAGGATTGGAGAGCCACTTGAGGTCATATGTT  |
| HC2C          | -----                                                        |
| HC2D-KIAA1058 | ATTCATGTGGTTGCCAGTGCCATGAGGAAGGATTGGAGAGCCACTTGAGGTCATATGTT  |
| HC2E          | ATTCATGTGGTTGCCAGTGCCATGAGGAAGGATTGGAGAGCCACTTGAGGTCATATGTT  |
| HC2F          | -----                                                        |
|               |                                                              |
| HC2A          | AAGTACGCGTATAAGGCTGAGCCATATGTTGCCTCTGAATACAAGACAGTGCATGAAGAA |
| HC2-80        | -----                                                        |
| HC2B          | AAGTACGCGTATAAGGCTGAGCCATATGTTGCCTCTGAATACAAGACAGTGCATGAAGAA |
| HC2C          | -----                                                        |
| HC2D-KIAA1058 | AAGTACGCGTATAAGGCTGAGCCATATGTTGCCTCTGAATACAAGACAGTGCATGAAGAA |
| HC2E          | AAGTACGCGTATAAGGCTGAGCCATATGTTGCCTCTGAATACAAGACAGTGCATGAAGAA |
| HC2F          | -----                                                        |
|               |                                                              |
| HC2A          | CTGACCAAATCCATGACCACGATTCTCAAGCCTTCTGCCGATTTCTCACCAGCAACAAA  |
| HC2-80        | -----                                                        |
| HC2B          | CTGACCAAATCCATGACCACGATTCTCAAGCCTTCTGCCGATTTCTCACCAGCAACAAA  |
| HC2C          | -----                                                        |
| HC2D-KIAA1058 | CTGACCAAATCCATGACCACGATTCTCAAGCCTTCTGCCGATTTCTCACCAGCAACAAA  |
| HC2E          | CTGACCAAATCCATGACCACGATTCTCAAGCCTTCTGCCGATTTCTCACCAGCAACAAA  |
| HC2F          | -----                                                        |
|               |                                                              |
| HC2A          | CTACTGAGGTACTCATGGTTTTTCTTTGATGTACTGATCAAATCTATGGCTCAGCATTTG |
| HC2-80        | -----                                                        |
| HC2B          | CTACTGAGGTACTCATGGTTTTTCTTTGATGTACTGATCAAATCTATGGCTCAGCATTTG |
| HC2C          | -----                                                        |
| HC2D-KIAA1058 | CTACTGAAGTACTCATGGTTTTTCTTTGATGTACTGATCAAATCTATGGCTCAGCATTTG |
| HC2E          | CTACTGAGGTACTCATGGTTTTTCTTTGATGTACTGATCAAATCTATGGCTCAGCATTTG |
| HC2F          | -----                                                        |
|               |                                                              |
| HC2A          | ATAGAGAACTCCAAAGTTAAGTTGCTGCGAAACCAGAGATTTCTTGCATCCTATCATCAT |
| HC2-80        | -----                                                        |
| HC2B          | ATAGAGAACTCCAAAGTTAAGTTGCTGCGAAACCAGAGATTTCTTGCATCCTATCATCAT |
| HC2C          | -----                                                        |
| HC2D-KIAA1058 | ATAGAGAACTCCAAAGTTAAGTTGCTGCGAAACCAGAGATTTCTTGCATCCTATCATCAT |
| HC2E          | ATAGAGAACTCCAAAGTTAAGTTGCTGCGAAACCAGAGATTTCTTGCATCCTATCATCAT |
| HC2F          | -----                                                        |

Fig. 3A (cont.)

|               |                                                               |
|---------------|---------------------------------------------------------------|
| HC2A          | GCAGCGGAAACCGTTGTAAATATGCTGATGCCACACATCACTCAGAAGTTTGGAGATAAT  |
| HC2-80        | -----                                                         |
| HC2B          | GCAGCGGAAACCGTTGTAAATATGCTGATGCCACACATCACTCAGAAGTTTGGAGATAAT  |
| HC2C          | -----                                                         |
| HC2D-KIAA1058 | GCAGTGGAAACCGTTGTAAATATGCTGATGCCACACATCACTCAGAAGTTTGGAGATAAT  |
| HC2E          | GCAGCGGAAACCGTTGTAAATATGCTGATGCCACACATCACTCAGAAGTTTGGAGATAAT  |
| HC2F          | -----                                                         |
|               |                                                               |
| HC2A          | CCAGAGGCATCTAAGAACGCGAATCATAGCCTTGCTGTCTTCATCAAGAGATGTTTCACC  |
| HC2-80        | -----                                                         |
| HC2B          | CCAGAGGCATCTAAGAACGCGAATCATAGCCTTGCTGTCTTCATCAAGAGATGTTTCACC  |
| HC2C          | -----                                                         |
| HC2D-KIAA1058 | CCAGAGGCATCTAAGAACGCGAATCATAGCCTTGCTGTCTTCATCAAGAGATGTTTCACC  |
| HC2E          | CCAGAGGCATCTAAGAACGCGAATCATAGCCTTGCTGTCTTCATCAAGAGATGTTTCACC  |
| HC2F          | -----                                                         |
|               |                                                               |
| HC2A          | TTCATGGACAGGGGCTTTGTCTTCAAGCAGATCAACAACCTACATTAGCTGTTTTGCTCCT |
| HC2-80        | -----                                                         |
| HC2B          | TTCATGGACAGGGGCTTTGTCTTCAAGCAGATCAACAACCTACATTAGCTGTTTTGCTCCT |
| HC2C          | -----                                                         |
| HC2D-KIAA1058 | TTCATGGACAGGGGCTTTGTCTTCAAGCAGATCAACAACCTACATTAGCTGTTTTGCTCCT |
| HC2E          | TTCATGGACAGGGGCTTTGTCTTCAAGCAGATCAACAACCTACATTAGCTGTTTTGCTCCT |
| HC2F          | -----                                                         |
|               |                                                               |
| HC2A          | GGAGACCCAAAGACCCTCTTTGAATACAAGTTTGAATTTCTCCGTGTAGTGTGCAACCAT  |
| HC2-80        | -----                                                         |
| HC2B          | GGAGACCCAAAGACCCTCTTTGAATACAAGTTTGAATTTCTCCGTGTAGTGTGCAACCAT  |
| HC2C          | -----                                                         |
| HC2D-KIAA1058 | GGAGACCCAAAGACCCTCTTTGAATACAAGTTTGAATTTCTCCGTGTAGTGTGCAACCAT  |
| HC2E          | GGAGACCCAAAGACCCTCTTTGAATACAAGTTTGAATTTCTCCGTGTAGTGTGCAACCAT  |
| HC2F          | -----                                                         |
|               |                                                               |
| HC2A          | GAACATTATATTCCGTTGAACTTACCAATGCCATTTGGAAAAGGCAGGATTCAAAGATAC  |
| HC2-80        | -----                                                         |
| HC2B          | GAACATTATATTCCGTTGAACTTACCAATGCCATTTGGAAAAGGCAGGATTCAAAGATAC  |
| HC2C          | -----                                                         |
| HC2D-KIAA1058 | GAACATTATATTCCGTTGAACTTACCAATGCCATTTGGAAAAGGCAGGATTCAAAGATAC  |
| HC2E          | GAACATTATATTCCGTTGAACTTACCAATGCCATTTGGAAAAGGCAGGATTCAAAGATAC  |
| HC2F          | -----                                                         |
|               |                                                               |
| HC2A          | CAAGACCTCCAGCTTGACTACTCATTAAACAGATGAGTTCTGCAGAAACCACTTCTTGGTG |
| HC2-80        | -----TCCAGCTTGACTACTCATTAAACAGATGAGTTCTGCAGAAACCACTTCTTGGTG   |
| HC2B          | CAAGACCTCCAGCTTGACTACTCATTAAACAGATGAGTTCTGCAGAAACCACTTCTTGGTG |
| HC2C          | -----                                                         |
| HC2D-KIAA1058 | CAAGACCTCCAGCTTGACTACTCATTAAACAGATGAGTTCTGCAGAAACCACTTCTTGGTG |
| HC2E          | CAAGACCTCCAGCTTGACTACTCATTAAACAGATGAGTTCTGCAGAAACCACTTCTTGGTG |
| HC2F          | -----                                                         |

FIG. 3A (cont.)

|               |                                                              |
|---------------|--------------------------------------------------------------|
| HC2A          | GGACTGTTACTGAGGGAGGTGGGGACAGCCCTCCAGGAGTTCCGGGAGGTCCGTCTGATC |
| HC2-80        | GGACTGTTACTGAGGGAGGTGGGGACAGCCCTCCAGGAGTTCCGGGAGGTCCGTCTGATC |
| HC2B          | GGACTGTTACTGAGGGAGGTGGGGACAGCCCTCCAGGAGTTCCGGGAGGTCCGTCTGATC |
| HC2C          | -----                                                        |
| HC2D-KIAA1058 | GGACTGTTACTGAGGGAGGTGGGGACAGCCCTCCAGGAGTTCCGGGAGGTCCGTCTGATC |
| HC2E          | GGACTGTTACTGAGGGAGGTGGGGACAGCCCTCCAGGAGTTCCGGGAGGTCCGTCTGATC |
| HC2F          | -----                                                        |
|               |                                                              |
| HC2A          | GCCATCAGTGTGCTCAAGAACCTGCTGATAAAGCATTCTTTTGATGACAGATATGCTTCA |
| HC2-80        | GCCATCAGTGTGCTCAAGAACCTGCTGATAAAGCATTCTTTTGATGACAGATATGCTTCA |
| HC2B          | GCCATCAGTGTGCTCAAGAACCTGCTGATAAAGCATTCTTTTGATGACAGATATGCTTCA |
| HC2C          | -----                                                        |
| HC2D-KIAA1058 | GCCATCAGTGTGCTCAAGAACCTGCTGATAAAGCATTCTTTTGATGACAGATATGCTTCA |
| HC2E          | GCCATCAGTGTGCTCAAGAACCTGCTGATAAAGCATTCTTTTGATGACAGATATGCTTCA |
| HC2F          | -----                                                        |
|               |                                                              |
| HC2A          | AGGAGCCATCAGGCAAGGATAGCCACCCTCTACCTGCCTCTGTTTGGTCTGCTGATTGAA |
| HC2-80        | AGGAGCCATCAGGCAAGGATAGCCACCCTCTACCTGCCTCTGTTTGGTCTGCTGATTGAA |
| HC2B          | AGGAGCCATCAGGCAAGGATAGCCACCCTCTACCTGCCTCTGTTTGGTCTGCTGATTGAA |
| HC2C          | -----                                                        |
| HC2D-KIAA1058 | AGGAGCCATCAGGCAAGGATAGCCACCCTCTACCTGCCTCTGTTTGGTCTGCTGATTGAA |
| HC2E          | AGGAGCCATCAGGCAAGGATAGCCACCCTCTACCTGCCTCTGTTTGGTCTGCTGATTGAA |
| HC2F          | -----                                                        |
|               |                                                              |
| HC2A          | AACGTCCAGCGGATCAATGTGAGGGATGTGTACCCCTTCCCTGTGAACGCGGGCATGACC |
| HC2-80        | AACGTCCAGCGGATCAATGTGAGGGATGTGTACCCCTTCCCTGTGAACGCGGGCATGACC |
| HC2B          | AACGTCCAGCGGATCAATGTGAGGGATGTGTACCCCTTCCCTGTGAACGCGGGCATGACC |
| HC2C          | -----                                                        |
| HC2D-KIAA1058 | AACGTCCAGCGGATCAATGTGAGGGATGTGTACCCCTTCCCTGTGAACGCGGGCATGACT |
| HC2E          | AACGTCCAGCGGATCAATGTGAGGGATGTGTACCCCTTCCCTGTGAACGCGGGCATGACC |
| HC2F          | -----                                                        |
|               |                                                              |
| HC2A          | GTGAAGGATGAATCCCTGGCTCTACCAGCTGTGAATCCGCTGGTGACGCCGAGAAGGGA  |
| HC2-80        | GTGAAGGATGAATCCCTGGCTCTACCAGCTGTGAATCCGCTGGTGACGCCGAGAAGGGA  |
| HC2B          | GTGAAGGATGAATCCCTGGCTCTACCAGCTGTGAATCCGCTGGTGACGCCGAGAAGGGA  |
| HC2C          | -----                                                        |
| HC2D-KIAA1058 | GTGAAGGATGAATCCCTGGCTCTACCAGCTGTGAATCCGCTGGTGACGCCGAGAAGGGA  |
| HC2E          | GTGAAGGATGAATCCCTGGCTCTACCAGCTGTGAATCCGCTGGTGACGCCGAGAAGGGA  |
| HC2F          | -----                                                        |
|               |                                                              |
| HC2A          | AGCACCTGGACAACAGCCTGCACAAGGACCTGCTGGGCGCCATCTCCGGCATTGCTTCT  |
| HC2-80        | AGCACCTGGACAACAGCCTGCACAAGGACCTGCTGGGCGCCATCTCCGGCATTGCTTCT  |
| HC2B          | AGCACCTGGACAACAGCCTGCACAAGGACCTGCTGGGCGCCATCTCCGGCATTGCTTCT  |
| HC2C          | -----                                                        |
| HC2D-KIAA1058 | AGCACCTGGACAACAGCCTGCACAAGGACCTGCTGGGCGCCATCTCCGGCATTGCTTCT  |
| HC2E          | AGCACCTGGACAACAGCCTGCACAAGGACCTGCTGGGCGCCATCTCCGGCATTGCTTCT  |
| HC2F          | -----                                                        |

|               |                                                               |
|---------------|---------------------------------------------------------------|
| HC2A          | CCATATACAACCTCAACTCCAAACATCAACAGTGTGAGAAATGCTGATTTCGAGAGGATCT |
| HC2-80        | CCATATACAACCTCAACTCCAAACATCAACAGTGTGAGAAATGCTGATTTCGAGAGGATCT |
| HC2B          | CCATATACAACCTCAACTCCAAACATCAACAGTGTGAGAAATGCTGATTTCGAGAGGATCT |
| HC2C          | -----                                                         |
| HC2D-KIAA1058 | CCATATACAACCTCAACTCCAAACATCAACAGTGTGAGAAATGCTGATTTCGAGAGGATCT |
| HC2E          | CCATATACAACCTCAACTCCAAACATCAACAGTGTGAGAAATGCTGATTTCGAGAGGATCT |
| HC2F          | -----GCTGATTTCGAGAGGATCT                                      |
|               |                                                               |
| HC2A          | CTCATAAGCACAGATTTCGGGTAACAGCCTTCCAGAAAGGAATAGTGAGAAGAGCAATTCC |
| HC2-80        | CTCATAAGCACAGATTTCGGGTAACAGCCTTCCAGAAAGGAATAGTGAGAAGAGCAATTCC |
| HC2B          | CTCATAAGCACAGATTTCGGGTAACAGCCTTCCAGAAAGGAATAGTGAGAAGAGCAATTCC |
| HC2C          | -----                                                         |
| HC2D-KIAA1058 | CTCATAAGCACAGATTTCGGGTAACAGCCTTCCAGAAAGGAATAGTGAGAAGAGCAATTCC |
| HC2E          | CTCATAAGCACAGATTTCGGGTAACAGCCTTCCAGAAAGGAATAGTGAGAAGAGCAATTCC |
| HC2F          | CTCATAAGCACAGATTTCGGGTAACAGCCTTCCAGAAAGGAATAGTGAGAAGAGCAATTCC |
|               |                                                               |
| HC2A          | CTGGATAAGCACCAACAAAGTAGCACATTGGGAAATTCCGTGGTTCGCTGTGATAAACTT  |
| HC2-80        | CTGGATAAGCACCAACAAAGTAGCACATTGGGAAATTCCGTGGTTCGCTGTGATAAACTT  |
| HC2B          | CTGGATAAGCACCAACAAAGTAGCACATTGGGAAATTCCGTGGTTCGCTGTGATAAACTT  |
| HC2C          | -----                                                         |
| HC2D-KIAA1058 | CTGGATAAGCACCAACAAAGTAGCACATTGGGAAATTCCGTGGTTCGCTGTGATAAACTT  |
| HC2E          | CTGGATAAGCACCAACAAAGTAGCACATTGGGAAATTCCGTGGTTCGCTGTGATAAACTT  |
| HC2F          | CTGGATAAGCACCAACAAAGTAGCACATTGGGAAATTCCGTGGTTCGCTGTGATAAACTT  |
|               |                                                               |
| HC2A          | GACCACTCTGAGATTAAGAGCCTACTGATGTGTTTCCTCTACATCTTAAAGAGCATGTCT  |
| HC2-80        | GACCACTCTGAGATTAAGAGCCTACTGATGTGTTTCCTCTACATCTTAAAGAGCATGTCT  |
| HC2B          | GACCACTCTGAGATTAAGAGCCTACTGATGTGTTTCCTCTACATCTTAAAGAGCATGTCT  |
| HC2C          | -----                                                         |
| HC2D-KIAA1058 | GACCACTCTGAGATTAAGAGCCTACTGATGTGTTTCCTCTACATCTTAAAGAGCATGTCT  |
| HC2E          | GACCACTCTGAGATTAAGAGCCTACTGATGTGTTTCCTCTACATCTTAAAGAGCATGTCT  |
| HC2F          | GACCACTCTGAGATTAAGAGCCTACTGATGTGTTTCCTCTACATCTTAAAGAGCATGTCT  |
|               |                                                               |
| HC2A          | GATGATGCTTTGTTTACATATTGGAACAAGGCTTCAACATCTGAACTTATGGATTTTTTTT |
| HC2-80        | GATGATGCTTTGTTTACATATTGGAACAAGGCTTCAACATCTGAACTTATGGATTTTTTTT |
| HC2B          | GATGATGCTTTGTTTACATATTGGAACAAGGCTTCAACATCTGAACTTATGGATTTTTTTT |
| HC2C          | -----                                                         |
| HC2D-KIAA1058 | GATGATGCTTTGTTTACATATTGGAACAAGGCTTCAACATCTGAACTTATGGATTTTTTTT |
| HC2E          | GATGATGCTTTGTTTACATATTGGAACAAGGCTTCAACATCTGAACTTATGGATTTTTTTT |
| HC2F          | GATGATGCTTTGTTTACATATTGGAACAAGGCTTCAACATCTGAACTTATGGATTTTTTTT |
|               |                                                               |
| HC2A          | ACAATATCTGAAGTCTGCCTGCACCAGTTCAGTACATGGGGAAGCGATACATAGCCAGG   |
| HC2-80        | ACAATATCTGAAGTCTGCCTGCACCAGTTCAGTACATGGGGAAGCGATACATAGCCAGG   |
| HC2B          | ACAATATCTGAAGTCTGCCTGCACCAGTTCAGTACATGGGGAAGCGATACATAGCCAGG   |
| HC2C          | -----                                                         |
| HC2D-KIAA1058 | ACAATATCTGAAGTCTGCCTGCACCAGTTCAGTACATGGGGAAGCGATACATAGCCAG-   |
| HC2E          | ACAATATCTGAAGTCTGCCTGCACCAGTTCAGTACATGGGGAAGCGATACATAGCCAGG   |
| HC2F          | ACAATATCTGAAGTCTGCCTGCACCAGTTCAGTACATGGGGAAGCGATACATAGCCAG-   |

Fig. 3A (cont.)

HC2A  
 HC2-80  
 HC2B  
 HC2C  
 HC2D-KIAA1058  
 HC2E  
 HC2F

AACCAGGAGGGGTTGGGACCCATAGTTCATGATCGAAAGTCTCAGACATTGCCTGTTTCC  
 AACCAGGAGGGGTTGGGACCCATAGTTCATGATCGAAAGTCTCAGACATTGCCTGTTTCC  
 AACCAGGAGGGGTTGGGACCCATAGTTCATGATCGAAAGTCTCAGACATTGCCTGTTTCC  
 -----  
 -----AA-----  
 AACCAGGAGGGGTTGGGACCCATAGTTCATGATCGAAAGTCTCAGACATTGCCTGTTTCC  
 -----TGTGA-----GAAAG-----ATATCAAGTGT-----

HC2A  
 HC2-80  
 HC2B  
 HC2C  
 HC2D-KIAA1058  
 HC2E  
 HC2F

CGTAACAGAACAGGAATGATGCATGCCAGATTGCAGCAGCTGGGCAGCCTGGATAACTCT  
 CGTAACAGAACAGGAATGATGCATGCCAGATTGCAGCAGCTGGGCAGCCTGGATAACTCT  
 CGTAACAGAACAGGAATGATGCATGCCAGATTGCAGCAGCTGGGCAGCCTGGATAACTCT  
 -----  
 -----CAGGAATGATGCATGCCAGATTGCAGCAGCTGGGCAGCCTGGATAACTCT  
 CGTAACAGAACAGGAATGATGCATGCCAGATTGCAGCAGCTGGGCAGCCTGGATAACTCT  
 -----GCTTGGA-----

HC2A  
 HC2-80  
 HC2B  
 HC2C  
 HC2D-KIAA1058  
 HC2E  
 HC2F

CTCACTTTTAACCACAGCTATGGCCACTCGGACGCAGATGTTCTGCACCAGTCATTACTT  
 CTCACCTTTTAACCACAGCTATGGCCACTCGGACGCAGATGTTCTGCACCAGTCATTACTT  
 CTCACCTTTTAACCACAGCTATGGCCACTCGGACGCAGATGTTCTGCACCAGTCATTACTT  
 -----  
 CTCACCTTTTAACCACAGCTATGGCCACTCGGACGCAGATGTTCTGCACCAGTCATTACTT  
 CTCACCTTTTAACCACAGCTATGGCCACTCGGACGCAGATGTTCTGCACCAGTCATTACTT  
 -TTTCTGTAGACAATGGCTATGGCCACTCGGACGCAGATGTTCTGCACCAGTCATTACTT

HC2A  
 HC2-80  
 HC2B  
 HC2C  
 HC2D-KIAA1058  
 HC2E  
 HC2F

GAAGCCAACATTGCTACTGAGGTTTGCCTGACAGCTCTGGACACGCTTTCTCTATTTACA  
 GAAGCCAACATTGCTACTGAGGTTTGCCTGACAGCTCTGGACACGCTTTCTCTATTTACA  
 GAAGCCAACATTGCTACTGAGGTTTGCCTGACAGCTCTGGACACGCTTTCTCTATTTACA  
 -----  
 GAAGCCAACATTGCTACTGAGGTTTGCCTGACAGCTCTGGACACGCTTTCTCTATTTACA  
 GAAGCCAACATTGCTACTGAGGTTTGCCTGACAGCTCTGGACACGCTTTCTCTATTTACA  
 GAAGCCAACATTGCTACTGAGGTTTGCCTGACAGCTCTGGACACGCTTTCTCTATTTACA

HC2A  
 HC2-80  
 HC2B  
 HC2C  
 HC2D-KIAA1058  
 HC2E  
 HC2F

TTGGCGTTTAAGAACCAGCTCCTGGCCGACCATGGACATAATCCTCTCATGAAAAAAGTT  
 TTGGCGTTTAAGAACCAGCTCCTGGCCGACCATGGACATAATCCTCTCATGAAAAAAGTT  
 TTGGCGTTTAAG-----CTCCTGGCCGACCATGGACATAATCCTCTCATGAAAAAAGTT  
 -----  
 TTGGCGTTTAAGAACCAGCTCCTGGCCGACCATGGACATAATCCTCTCATGAAAAAAGTT  
 TTGGCGTTTAAGAACCAGCTCCTGGCCGACCATGGACATAATCCTCTCATGAAAAAAGTT  
 TTGGCGTTTAAGAACCAGCTCCTGGCCGACCATGGACATAATCCTCTCATGAAAAAAGTT

HC2A  
 HC2-80  
 HC2B  
 HC2C  
 HC2D-KIAA1058  
 HC2E  
 HC2F

TTTGATGTCTACCTGTGTTTTCTTCAAAAACATCAGTCTGAAACGGCTTTAAAAAATGTC  
 TTTGATGTCTACCTGTGTTTTCTTCAAAAACATCAGTCTGAAACGGCTTTAAAAAATGTC  
 TTTGATGTCTACCTGTGTTTTCTTCAAAAACATCAGTCTGAAACGGCTTTAAAAAATGTC  
 -----  
 TTTGATGTCTACCTGTGTTTTCTTCAAAAACATCAGTCTGAAACGGCTTTAAAAAATGTC  
 TTTGATGTCTACCTGTGTTTTCTTCAAAAACATCAGTCTGAAACGGCTTTAAAAAATGTC  
 A-----

Fig. 3A (cont.)

09587837 101300

HC2A TTCACTGCCTTAAGGTCCTTAATTTATAAGTTTCCCTCAACATTCTATGAAGGGAGAGCG  
HC2-80 TTCACTGCCTTAAGGTCCTTAATTTATAAGTTTCCCTCAACATTCTATGAAGGGAGAGCG  
HC2B TTCACTGCCTTAAGGTCCTTAATTTATAAGTTTCCCTCAACATTCTATGAAGGGAGAGCG  
HC2C -----  
HC2D-KIAA1058 TTCACTGCCTTAAGGTCCTTAATTTATAAGTTTCCCTCAACATTCTATGAAGGGAGAGCG  
HC2E TTCACTGCCTTAAGGTCCTTAATTTATAAGTTTCCCTCAACATTCTATGAAGGGAGAGCG  
HC2F -----

HC2A GACATGTGTGCGGCTCTGTGTTACGAGATTCTCAAGTGCTGTAACCTCAAGCTGAGCTCC  
HC2-80 GACATGTGTGCGGCTCTGTGTTACGAGATTCTCAAGTGCTGTAACCTCAAGCTGAGCTCC  
HC2B GACATGTGTGCGGCTCTGTGTTACGAGATTCTCAAGTGCTGTAACCTCAAGCTGAGCTCC  
HC2C -----  
HC2D-KIAA1058 GACATGTGTGCGGCTCTGTGTTACGAGATTCTCAAGTGCTGTAACCTCAAGCTGAGCTCC  
HC2E GACATGTGTGCGGCTCTGTGTTACGAGATTCTCAAGTGCTGTAACCTCAAGCTGAGCTCC  
HC2F -----

HC2A ATCAGGACGGAGGCCTCCAGCTGCTCTACTTCCTGATGAGGAACAACCTTTGATTACACT  
HC2-80 ATCAGGACGGAGGCCTCCAGCTGCTCTACTTCCTGATGAGGAACAACCTTTGATTACACT  
HC2B ATCAGGACGGAGGCCTCCAGCTGCTCTACTTCCTGATGAGGAACAACCTTTGATTACACT  
HC2C -----  
HC2D-KIAA1058 ATCAGGACGGAGGCCTCCAGCTGCTCTACTTCCTGATGAGGAACAACCTTTGATTACACT  
HC2E ATCAGGACGGAGGCCTCCAGCTGCTCTACTTCCTGATGAGGAACAACCTTTGATTACACT  
HC2F -----

HC2A GGAAAGAAGTCCTTTGTCCGGACACATTTGCAAGTCATCATATCTGTCAGCCAGCTGATA  
HC2-80 GGAAAGAAGTCCTTTGTCCGGACACATTTGCAAGTCATCATATCTGTCAGCCAGCTGATA  
HC2B GGAAAGAAGTCCTTTGTCCGGACACATTTGCAAGTCATCATATCTGTCAGCCAGCTGATA  
HC2C -----  
HC2D-KIAA1058 GGAAAGAAGTCCTTTGTCCGGACACATTTGCAAGTCATCATATCTGTCAGCCAGCTGATA  
HC2E GGAAAGAAGTCCTTTGTCCGGACACATTTGCAAGTCATCATATCTGTCAGCCAGCTGATA  
HC2F -----

HC2A GCAGACGTTGTTGGCATTGGGGAAACCAGATTCCAGCAGTCCCTGTCCATCATCAACAAC  
HC2-80 GCAGACGTTGTTGGCATTGGGGAAACCAGATTCCAGCAGTCCCTGTCCATCATCAACAAC  
HC2B GCAGACGTTGTTGGCATTGGGGAAACCAGATTCCAGCAGTCCCTGTCCATCATCAACAAC  
HC2C -----  
HC2D-KIAA1058 GCAGACGTTGTTGGCATTGGGGAAACCAGATTCCAGCAGTCCCTGTCCATCATCAACAAC  
HC2E GCAGACGTTGTTGGCATTGGGGAAACCAGATTCCAGCAGTCCCTGTCCATCATCAACAAC  
HC2F -----

HC2A TGTGCCAACAGTGACCGGCTTATTAAGCACACCAGCTTCTCCTCTGATGTGAAGGACTTA  
HC2-80 TGTGCCAACAGTGACCGGCTTATTAAGCACACCAGCTTCTCCTCTGATGTGAAGGACTTA  
HC2B TGTGCCAACAGTGACCGGCTTATTAAGCACACCAGCTTCTCCTCTGATGTGAAGGACTTA  
HC2C -----  
HC2D-KIAA1058 TGTGCCAACAGTGACCGGCTTATTAAGCACACCAGCTTCTCCTCTGATGTGAAGGACTTA  
HC2E TGTGCCAACAGTGACCGGCTTATTAAGCACACCAGCTTCTCCTCTGATGTGAAGGACTTA  
HC2F -----

Fig. 3A (cont.)

|               |                                                              |
|---------------|--------------------------------------------------------------|
| HC2A          | ACCAAAAGGATACGCACGGTGCTAATGGCCACCGCCCAGATGAAGGAGCATGAGAACGAC |
| HC2-80        | ACCAAAAGGATACGCACGGTGCTAATGGCCACCGCCCAGATGAAGGAGCATGAGAACGAC |
| HC2B          | ACCAAAAGGATACGCACGGTGCTAATGGCCACCGCCCAGATGAAGGAGCATGAGAACGAC |
| HC2C          | -----                                                        |
| HC2D-KIAA1058 | ACCAAAAGGATACGCACGGTGCTAATGGCCACCGCCCAGATGAAGGAGCATGAGAACGAC |
| HC2E          | ACCAAAAGGATACGCACGGTGCTAATGGCCACCGCCCAGATGAAGGAGCATGAGAACGAC |
| HC2F          | -----                                                        |

|               |                                                               |
|---------------|---------------------------------------------------------------|
| HC2A          | CCAGAGATGCTGGTGGACCTCCAGTACAGCCTGGCCAAATCCTATGCCAGCACGCCCCGAG |
| HC2-80        | CCAGAGATGCTGGTGGACCTCCAGTACAGCCTGGCCAAATCCTATGCCAGCACGCCCCGAG |
| HC2B          | CCAGAGATGCTGGTGGACCTCCAGTACAGCCTGGCCAAATCCTATGCCAGCACGCCCCGAG |
| HC2C          | -----                                                         |
| HC2D-KIAA1058 | CCAGAGATGCTGGTGGACCTCCAGTACAGCCTGGCCAAATCCTATGCCAGCACGCCCCGAG |
| HC2E          | CCAGAGATGCTGGTGGACCTCCAGTACAGCCTGGCCAAATCCTATGCCAGCACGCCCCGAG |
| HC2F          | -----                                                         |

|               |                                                              |
|---------------|--------------------------------------------------------------|
| HC2A          | CTCAGGAAGACGTGGCTCGACAGCATGGCCAGGATCCATGTCAAAAATGGCGATCTCTCA |
| HC2-80        | CTCAGGAAGACGTGGCTCGACAGCATGGCCAGGATCCATGTCAAAAATGGCGATCTCTCA |
| HC2B          | CTCAGGAAGACGTGGCTCGACAGCATGGCCAGGATCCATGTCAAAAATGGCGATCTCTCA |
| HC2C          | -----                                                        |
| HC2D-KIAA1058 | CTCAGGAAGACGTGGCTCGACAGCATGGCCAGGATCCATGTCAAAAATGGCGATCTCTCA |
| HC2E          | CTCAGGAAGACGTGGCTCGACAGCATGGCCAGGATCCATGTCAAAAATGGCGATCTCTCA |
| HC2F          | -----                                                        |

|               |                                                              |
|---------------|--------------------------------------------------------------|
| HC2A          | GAGGCAGCAATGTGCTATGTCCACGTAACAGCCCTAGTGGCAGAATATCTCACACGGAAA |
| HC2-80        | GAGGCAGCAATGTGCTATGTCCACGTAACAGCCCTAGTGGCAGAATATCTCACACGGAAA |
| HC2B          | GAGGCAGCAATGTGCTATGTCCACGTAACAGCCCTAGTGGCAGAATATCTCACACGGAAA |
| HC2C          | -----                                                        |
| HC2D-KIAA1058 | GAGGCAGCAATGTGCTATGTCCACGTAACAGCCCTAGTGGCAGAATATCTCACACGGAAA |
| HC2E          | GAGGCAGCAATGTGCTATGTCCACGTAACAGCCCTAGTGGCAGAATATCTCACACGGAAA |
| HC2F          | -----                                                        |

|               |                                                            |
|---------------|------------------------------------------------------------|
| HC2A          | G-----                                                     |
| HC2-80        | G-----                                                     |
| HC2B          | G-----                                                     |
| HC2C          | -----                                                      |
| HC2D-KIAA1058 | GAAGCAGTCCAGTGGGAGCCGCCCTTCTCCCCACAGCCATAGCGCCTGCCTGAGGAGG |
| HC2E          | G-----                                                     |
| HC2F          | -----                                                      |

|               |                                                               |
|---------------|---------------------------------------------------------------|
| HC2A          | -----GCGTGTTTAGACAAGGATGCACCGCCTTCAGGGTCATTACCCCCAAACATC      |
| HC2-80        | -----GCGTGTTTAGACAAGGATGCACCGCCTTCAGGGTCATTACCCCCAAACATC      |
| HC2B          | -----GCGTGTTTAGACAAGGATGCACCGCCTTCAGGGTCATTACCCCCAAACATC      |
| HC2C          | -----GTTTAGACAAGGATGCACCGCCTTCAGGGTCATTACCCCCAAACATC          |
| HC2D-KIAA1058 | AGCCGGGGAGGCGTGTTTAGACAAGGATGCACCGCCTTCAGGGTCATTACCCCCAAACATC |
| HC2E          | -----GCGTGTTTAGACAAGGATGCACCGCCTTCAGGGTCATTACCCCCAAACATC      |
| HC2F          | -----                                                         |

FIG. 3A (cont.)



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|               |                                                              |
|---------------|--------------------------------------------------------------|
| HC2A          | GACGAGGAGGCCTCCATGATGGAAGACGTGGGGATGCAGGATGTCCATTTCAACGAGGAT |
| HC2-80        | GACGAGGAGGCCTCCATGATGGAAGACGTGGGGATGCAGGATGTCCATTTCAACGAGGAT |
| HC2B          | GACGAGGAGGCCTCCATGATGGAAGACGTGGGGATGCAGGATGTCCATTTCAACGAGGAT |
| HC2C          | GACGAGGAGGCCTCCATGATGGAAGACGTGGGGATGCAGGATGTCCATTTCAACGAGGAT |
| HC2D-KIAA1058 | GACGAGGAGGCCTCCATGATGGAAGACGTGGGGATGCAGGATGTCCATTTCAACGAGGAT |
| HC2E          | GACGAGGAGGCCTCCATGATGGAAGACGTGGGGA-----                      |
| HC2F          | -----                                                        |
|               |                                                              |
| HC2A          | GTGCTGATGGAGCTCCTTGAGCAGTGCGCAGATGGACTCTGGAAAGCCGAGCGCTACGAG |
| HC2-80        | GTGCTGATGGAGCTCCTTGAGCAGTGCGCAGATGGACTCTGGAAAGCCGAGCGCTACGAG |
| HC2B          | GTGCTGATGGAGCTCCTTGAGCAGTGCGCAGATGGACTCTGGAAAGCCGAGCGCTACGAG |
| HC2C          | GTGCTGATGGAGCTCCTTGAGCAGTGCGCAGATGGACTCTGGAAAGCCGAGCGCTACGAG |
| HC2D-KIAA1058 | GTGCTGATGGAGCTCCTTGAGCAGTGCGCAGATGGACTCTGGAAAGCCGAGCGCTACGAG |
| HC2E          | -----AAGCCGAGCGCTACGAG                                       |
| HC2F          | -----                                                        |
|               |                                                              |
| HC2A          | CTCATCGCCGACATCTACAACTTATCATCCCCATTTATGAGAAGCGGAGGGATTT----  |
| HC2-80        | CTCATCGCCGACATCTACAACTTATCATCCCCATTTATGAGAAGCGGAGGGATTT----  |
| HC2B          | CTCATCGCCGACATCTACAACTTATCATCCCCATTTATGAGAAGCGGAGGGATTTTGAG  |
| HC2C          | CTCATCGCCGACATCTACAACTTATCATCCCCATTTATGAGAAGCGGAGGGATTTTGAG  |
| HC2D-KIAA1058 | CTCATTGCGGACATCTACAACTTATCATCCCCATTTATGAGAAGCGGAGGGATTTTGAG  |
| HC2E          | CTCATCGCCGACATCTACAACTTATCATCCCCATTTATGAGAAGCGGAGGGATTTTGAG  |
| HC2F          | -----                                                        |
|               |                                                              |
| HC2A          | -----                                                        |
| HC2-80        | -----                                                        |
| HC2B          | AGGCTGGCCCATCTGTATGACACGCTGCACCGGGCCTACAGCAAAGTGACCGAGGTCATG |
| HC2C          | AGGCTGGCCCATCTGTATGACACGCTGCACCGGGCCTACAGCAAAGTGACCGAGGTCATG |
| HC2D-KIAA1058 | AGGCTGGCCCATCTGTATGACACGCTGCACCGGGCCTACAGCAAAGTGACCGAGGTCATG |
| HC2E          | AGGCTGGCCCATCTGTATGACACGCTGCACCGGGCCTACAGCAAAGTGACCGAGGTCATG |
| HC2F          | -----                                                        |
|               |                                                              |
| HC2A          | -----                                                        |
| HC2-80        | -----                                                        |
| HC2B          | CACTCGGGCCGAGGCTTCTGGGGACCTACTTCCGGGTAGCCTTCTTCGGGCAGG----   |
| HC2C          | CACTCGGGCCGAGGCTTCTGGGGACCTACTTCCGGGTAGCCTTCTTCGGGCAGG----   |
| HC2D-KIAA1058 | CACTCGGGCCGAGGCTTCTGGGGACCTACTTCCGGGTAGCCTTCTTCGGGCAGGCAGCG  |
| HC2E          | CACTCGGGCCGAGGCTTCTGGGGACCTACTTCCGGGTAGCCTTCTTCGGGCAGG----   |
| HC2F          | -----                                                        |
|               |                                                              |
| HC2A          | -----CTTTGAAGATGAAGATGGA                                     |
| HC2-80        | -----CTTTGAAGATGAAGATGGA                                     |
| HC2B          | -----GATTCTTTGAAGATGAAGATGGA                                 |
| HC2C          | -----GATTCTTTGAAGATGAAGATGGA                                 |
| HC2D-KIAA1058 | CAATACCAGTTTACAGACAGTGAAACAGATGTGGAGGGATTCTTTGAAGATGAAGATGGA |
| HC2E          | -----GATTCTTTGAAGATGAAGATGGA                                 |
| HC2F          | -----                                                        |

Fig. 3A (cont.)

HC2A  
HC2-80  
HC2B  
HC2C  
HC2D-KIAA1058  
HC2E  
HC2F

AAGGAGTATATTTACAAGGAACCCAAACTCACACCGCTGTCGGAAATTTCTCAGAGACTC  
AAGGAGTATATTTACAAGGAACCCAAACTCACACCGCTGTCGGAAATTTCTCAGAGACTC  
AAGGAGTATATTTACAAGGAACCCAAACTCACACCGCTGTCGGAAATTTCTCAGAGACTC  
AAGGAGTATATTTACAAGGAACCCAAACTCACACCGCTGTCGGAAATTTCTCAGAGACTC  
AAGGAGTATATTTACAAGGAACCCAAACTCACACCGCTGTCGGAAATTTCTCAGAGACTC  
AAGGAGTATATTTACAAGGAACCCAAACTCACACCGCTGTCGGAAATTTCTCAGAGACTC  
-----

HC2A  
HC2-80  
HC2B  
HC2C  
HC2D-KIAA1058  
HC2E  
HC2F

CTTAAACTGTACTCGGATAAATTTGGTTCTGAAAATGTCAAATGATACAGGATTCTGGC  
CTTAAACTGTACTCGGATAAATTTGGTTCTGAAAATGTCAAATGATACAGGATTCTGGC  
CTTAAACTGTACTCGGATAAATTTGGTTCTGAAAATGTCAAATGATACAGGATTCTGGC  
CTTAAACTGTACTCGGATAAATTTGGTTCTGAAAATGTCAAATGATACAGGATTCTGGC  
CTTAAACTGTACTCGGATAAATTTGGTTCTGAAAATGTCAAATGATACAGGATTCTGGC  
CTTAAACTGTACTCGGATAAATTTGGTTCTGAAAATGTCAAATGATACAGGATTCTGGC  
-----

HC2A  
HC2-80  
HC2B  
HC2C  
HC2D-KIAA1058  
HC2E  
HC2F

AAGGTCAACCCTAAGGATCTGGATTCTAAGTATGCATACATCCAGGTGACTCACGTCATC  
AAGGTCAACCCTAAGGATCTGGATTCTAAGTATGCATACATCCAGGTGACTCACGTCATC  
AAGGTCAACCCTAAGGATCTGGATTCTAAGTATGCATACATCCAGGTGACTCACGTCATC  
AAGGTCAACCCTAAGGATCTGGATTCTAAGTATGCATACATCCAGGTGACTCACGTCATC  
AAGGTCAACCCTAAGGATCTGGATTCTAAGTATGCCTACATCCAGGTGACTCACGTCATC  
AAGGTCAACCCTAAGGATCTGGATTCTAAGTATGCATACATCCAGGTGACTCACGTCATC  
-----

HC2A  
HC2-80  
HC2B  
HC2C  
HC2D-KIAA1058  
HC2E  
HC2F

CCCTTCTTTGACGAAAAAGAGTTGCAAGAAAGGAAAAACAGAGTTTGAGAGATCCCACAAC  
CCCTTCTTTGACGAAAAAGAGTTGCAAGAAAGGAAAAACAGAGTTTGAGAGATCCCACAAC  
CCCTTCTTTGACGAAAAAGAGTTGCAAGAAAGGAAAAACAGAGTTTGAGAGATCCCACAAC  
CCCTTCTTTGACGAAAAAGAGTTGCAAGAAAGGAAAAACAGAGTTTGAGAGATCCCACAAC  
CCCTTCTTTGACGAAAAAGAGTTGCAAGAAAGGAAAAACAGAGTTTGAGAGATCCCACAAC  
CCCTTCTTTGACGAAAAAGAGTTGCAAGAAAGGAAAAACAGAGTTTGAGAGATCCCACAAC  
-----

HC2A  
HC2-80  
HC2B  
HC2C  
HC2D-KIAA1058  
HC2E  
HC2F

ATCCGCCGCTTCATGTTTGAGATGCCATTTACGCAGACCGGGAAGAGGCAGGGCGGGGTG  
ATCCGCCGCTTCATGTTTGAGATGCCATTTACGCAGACCGGGAAGAGGCAGGGCGGGGTG  
ATCCGCCGCTTCATGTTTGAGATGCCATTTACGCAGACCGGGAAGAGGCAGGGCGGGGTG  
ATCCGCCGCTTCATGTTTGAGATGCCATTTACGCAGACCGGGAAGAGGCAGGGCGGGGTG  
ATCCGCCGCTTCATGTTTGAGATGCCATTTACGCAGACCGGGAAGAGGCAGGGCGGGGTG  
ATCCGCCGCTTCATGTTTGAGATGCCATTTACGCAGACCGGGAAGAGGCAGGGCGGGGTG  
-----

HC2A  
HC2-80  
HC2B  
HC2C  
HC2D-KIAA1058  
HC2E  
HC2F

GAAGAGCAGTGCAAACGGCGCACCATCCTGACAGCCATACACTGCTTCCCTTATGTGAAG  
GAAGAGCAGTGCAAACGGCGCACCATCCTGACAGCCATACACTGCTTCCCTTATGTGAAG  
GAAGAGCAGTGCAAACGGCGCACCATCCTGACAGCCATACACTGCTTCCCTTATGTGAAG  
GAAGAGCAGTGCAAACGGCGCACCATCCTGACAGCCATACACTGCTTCCCTTATGTGAAG  
GAAGAGCAGTGCAAACGGCGCACCATCCTGACAGCCATACACTGCTTCCCTTATGTGAAG  
GAAGAGCAGTGCAAACGGCGCACCATCCTGACAGCCATACACTGCTTCCCTTATGTGAAG  
-----

Fig. 3A (cont.)

|               |                                                               |
|---------------|---------------------------------------------------------------|
| HC2A          | AAGCGCATCCCTGTCATGTACCAGCACCACACTGACCTGAACCCCATCGAGGTGGCCATT  |
| HC2-80        | AAGCGCATCCCTGTCATGTACCAGCACCACACTGACCTGAACCCCATCGAGGTGGCCATT  |
| HC2B          | AAGCGCATCCCTGTCATGTACCAGCACCACACTGACCTGAACCCCATCGAGGTGGCCATT  |
| HC2C          | AAGCGCATCCCTTTTCATGTACCAGCACCACACTGACCTGAACCCCATCGAGGT--CCATT |
| HC2D-KIAA1058 | AAGCGCATCCCTGTCATGTACCAGCACCACACTGACCTGAACCCCATCGAGGTGGCCATT  |
| HC2E          | AAGCGCATCCCTGTCATGTACCAGCACCACACTGACCTGAACCCCATCGAGGTGGCCATT  |
| HC2F          | -----                                                         |

|               |                                                              |
|---------------|--------------------------------------------------------------|
| HC2A          | GACGAGATGAGTAAGAAGGTGGCGGAGCTCCGGCAGCTGTGCTCCTCGGCCGAGGTGGAC |
| HC2-80        | GACGAGATGAGTAAGAAGGTGGCGGAGCTCCGGCAGCTGTGCTCCTCGGCCGAGGTGGAC |
| HC2B          | GACGAGATGAGTAAGAAGGTGGCGGAGCTCCGGCAGCTGTGCTCCTCGGCCGAGGTGGAC |
| HC2C          | GACGAGATGAGTAAGAAGGTGGCGGAGCTCCGGCAGCTGTGCTCCTCGGCCGAGGTGGAC |
| HC2D-KIAA1058 | GACGAGATGAGTAAGAAGGTGGCGGAGCTCCGGCAGCTGTGCTCCTCGGCCGAGGTGGAC |
| HC2E          | GACGAGATGAGTAAGAAGGTGGCGGAGCTCCGGCAGCTGTGCTCCTCGGCCGAGGTGGAC |
| HC2F          | -----                                                        |

|               |                                                                |
|---------------|----------------------------------------------------------------|
| HC2A          | ATGATCAAACCTGCAGCTCAAACCTCCAGGGCAGCGTGAGTGTTCAAGTCAATGCTGGCCCA |
| HC2-80        | ATGATCAAACCTGCAGCTCAAACCTCCAGGGCAGCGTGAGTGTTCAAGTCAATGCTGGCCCA |
| HC2B          | ATGATCAAACCTGCAGCTCAAACCTCCAGGGCAGCGTGAGTGTTCAAGTCAATGCTGGCCCA |
| HC2C          | ATGATCAAACCTGCAGCTCAAACCTCCAGGGCAGCGTGAGTGTTCAAGTCAATGCTGGCCCA |
| HC2D-KIAA1058 | ATGATCAAACCTGCAGCTCAAACCTCCAGGGCAGCGTGAGTGTTCAAGTCAATGCTGGCCCA |
| HC2E          | ATGATCAAACCTGCAGCTCAAACCTCCAGGGCAGCGTGAGTGTTCAAGTCAATGCTGGCCCA |
| HC2F          | -----                                                          |

|               |                                                              |
|---------------|--------------------------------------------------------------|
| HC2A          | CTAGCATATGCGCGAGCTTTCTTAGATGATACAAACACAAAGCGATATCCTGACAATAAA |
| HC2-80        | CTAGCATATGCGCGAGCTTTCTTAGATGATACAAACACAAAGCGATATCCTGACAATAAA |
| HC2B          | CTAGCATATGCGCGAGCTTTCTTAGATGATACAAACACAAAGCGATATCCTGACAATAAA |
| HC2C          | CTAGCATATGCGCGAGCTTTCTTAGATGATACAAACACAAAGCGATATCCTGACAATAAA |
| HC2D-KIAA1058 | CTAGCATATGCGCGAGCTTTCTTAGATGATACAAACACAAAGCGATATCCTGACAATAAA |
| HC2E          | CTAGCATATGCGCGAGCTTTCTTAGATGATACAAACACAAAGCGATATCCTGACAATAAA |
| HC2F          | -----                                                        |

|               |                                                               |
|---------------|---------------------------------------------------------------|
| HC2A          | GTGAAGCTGCTTAAGGAAGTTTTTCAGGCAATTTGTGGAAGCTTGCGGTCAAGCCTTAGCG |
| HC2-80        | GTGAAGCTGCTTAAGGAAGTTTTTCAGGCAATTTGTGGAAGCTTGCGGTCAAGCCTTAGCG |
| HC2B          | GTGAAGCTGCTTAAGGAAGTTTTTCAGGCAATTTGTGGAAGCTTGCGGTCAAGCCTTAGCG |
| HC2C          | GTGAAGCTGCTTAAGGAAGTTTTTCAGGCAATTTGTGGAAGCTTGCGGTCAAGCCTTAGCG |
| HC2D-KIAA1058 | GTGAAGCTGCTTAAGGAAGTTTTTCAGGCAATTTGTGGAAGCTTGCGGTCAAGCCTTAGCG |
| HC2E          | GTGAAGCTGCTTAAGGAAGTTTTTCAGGCAATTTGTGGAAGCTTGCGGTCAAGCCTTAGCG |
| HC2F          | -----                                                         |

|               |                                                              |
|---------------|--------------------------------------------------------------|
| HC2A          | GTAAACGAACGTCTGATTAAAGAAGACCAGCTCGAGTATCAGGAAGAAATGAAAGCCAAC |
| HC2-80        | GTAAACGAACGTCTGATTAAAGAAGACCAGCTCGAGTATCAGGAAGAAATGAAAGCCAAC |
| HC2B          | GTAAACGAACGTCTGATTAAAGAAGACCAGCTCGAGTATCAGGAAGAAATGAAAGCCAAC |
| HC2C          | GTAAACGAACGTCTGATTAAAGAAGACCAGCTCGAGTATCAGGAAGAAATGAAAGCCAAC |
| HC2D-KIAA1058 | GTAAACGAACGTCTGATTAAAGAAGACCAGCTCGAGTATCAGGAAGAAATGAAAGCCAAC |
| HC2E          | GTAAACGAACGTCTGATTAAAGAAGACCAGCTCGAGTATCAGGAAGAAATGAAAGCCAAC |
| HC2F          | -----                                                        |

HC2A  
HC2-80  
HC2B  
HC2C  
HC2D-KIAA1058  
HC2E  
HC2F

TACAGGGAAATGGCGAAGGAGCTTTCTGAAATCATGCATGAGCAG-----ATCTGCC  
TACAGGGAAATGGCGAAGGAGCTTTCTGAAATCATGCATGAGCAG-----ATCTGCC  
TACAGGGAAATGGCGAAGGAGCTTTCTGAAATCATGCATGAGCAG-----ATCTGCC  
TACAGGGAAATGGCGAAGGAGCTTTCTGAAATCATGCATGAGCAG-----ATCTGCC  
TACAGGGAAATGGCGAAGGAGCTTTCTGAAATCATGCATGAGCAGCTGGGATGATCTGCC  
TACAGGGAAATGGCGAAGGAGCTTTCTGAAATCATGCATGAGCAG-----ATCTGCC  
-----

HC2A  
HC2-80  
HC2B  
HC2C  
HC2D-KIAA1058  
HC2E  
HC2F

CCCTGGAGGAGAAGACGAGCGTCTTACCGAATTCCCTTCACATCTTCAACGCCATCAGTG  
CCCTGGAGGAGAAGACGAGCGTCTTACCGAATTCCCTTCACATCTTCAACGCCATCAGTG  
CCCTGGAGGAGAAGACGAGCGTCTTACCGAATTCCCTTCACATCTTCAACGCCATCAGTG  
CCCTGGAGGAGAAGACGAGCGTCTTACCGAATTCCCTTCACATCTTCAACGCCATCAGTG  
CCCTGGAGGAGAAGACGAGCGTCTTACCGAATTCCCTTCACATCTTCAACGCCATCAGTG  
CCCTGGAGGAGAAGACGAGCGTCTTACCGAATTCCCTTCACATCTTCAACGCCATCAGTG  
-----

HC2A  
HC2-80  
HC2B  
HC2C  
HC2D-KIAA1058  
HC2E  
HC2F

GGACTCCAACAAGCACAAATGGTTCACGGGATGACCAGCTCGTCTTCGGTCGTGTGATTAC  
GGACTCCAACAAGCACAAATGGTTCACGGGATGACCAGCTCGTCTTCGGTCGTGTGATTAC  
GGACTCCAACAAGCACAAATGGTTCACGGGATGACCAGCTCGTCTTCGGTCGTGTGA-----  
GGACTCCAACAAGCACAAATGGTTCACGGGATGACCAGCTCGTCTTCGGTCGTGTGA-----  
GGACTCCAACAAGCACAAATGGTTCACGGGATGACCAGCTCGTCTTCGGTCGTGTGATTAC  
GGACTCCAACAAGCACAAATGGTTCACGGGATGACCAGCTCGTCTTCGGTCGTGTGA-----  
-----

HC2A  
HC2-80  
HC2B  
HC2C  
HC2D-KIAA1058  
HC2E  
HC2F

ATCTCATGGCCCGTGTGTGGGGACTTGCTTTGTCAATTTGCAAACCTCAGGATGCTTTCCAA  
ATCTCATGGCCCGTGTGTGGGGACTTGCTTTGTCAATTTGCAAACCTCAGGATGCTTTCCAA  
-----  
-----  
ATCTCATGGCCCGTGTGTGGGGACTTGCTTTGTCAATTTGCAAACCTCAGGATGCTTTCCAA  
-----  
-----

HC2A  
HC2-80  
HC2B  
HC2C  
HC2D-KIAA1058  
HC2E  
HC2F

AGCCAATCACTGGGGAGACCGAGCACAGGGAGGACCAAGGGGAAGGGGAGAGAAAGGAAA  
AGCCAATCACTGGGGAGACCGAGCACAGGGAGGACCAAGGGGAAGGGGAGAGAAAGGAAA  
-----  
-----  
AGCCAATCACTGGGGAGACCGAGCACAGGGAGGACCA-GGGGAAGGGGAGAGAAAGGAAA  
-----  
-----

HC2A  
HC2-80  
HC2B  
HC2C  
HC2D-KIAA1058  
HC2E  
HC2F

TAAAGAACAACGTTATTTCTTAACAGACTTTCTATAGGAGTTGTAAGAAGGTGCACATAT  
TAAAGAACAACGTTATTTCTTAACAGACTTTCTATAGGAGTTGTAAGAAGGTGCACATAT  
-----  
-----  
TAAAGAACAACGTTATTTCTTAACAGACTTTCTATAGGAGTTGTAAGAAGGTGCACATAT  
-----  
-----

Fig. 3A (cont.)

|               |                                                               |
|---------------|---------------------------------------------------------------|
| HC2A          | TTTTTTAAATCTCACTGGCAATATTCAAAGTTTTTCATTGTGTCTTAACAAAGGTGTGGTA |
| HC2-80        | TTTTTTAAATCTCACTGGCAATATTCAAAGTTTTTCATTGTGTCTTAACAAAGGTGTGGTA |
| HC2B          | -----                                                         |
| HC2C          | -----                                                         |
| HC2D-KIAA1058 | TTTTTTAAATCTCACTGGCAATATTCAAAGTTTTTCATTGTGTCTTAACAAAGGTGTGGTA |
| HC2E          | -----                                                         |
| HC2F          | -----                                                         |

|               |                                                                |
|---------------|----------------------------------------------------------------|
| HC2A          | GACACTCTTGAGCTGGACTTAGATTTTTATTCTTCCTTGACAGAGTAGTGTTAGAATAGATG |
| HC2-80        | GACACTCTTGAGCTGGACTTAGATTTTTATTCTTCCTTGACAGAGTAGTGTTAGAATAGATG |
| HC2B          | -----                                                          |
| HC2C          | -----                                                          |
| HC2D-KIAA1058 | GACACTCTTGAGCTGGACTTAGATTTTTATTCTTCCTTGACAGAGTAGTGTTAGAATAGATG |
| HC2E          | -----                                                          |
| HC2F          | -----                                                          |

|               |                                                            |
|---------------|------------------------------------------------------------|
| HC2A          | GCCTACAGAAAAAAGGTTCTGGGATCTACATGGCAGGGAGGGCTGCACTGACATTGAT |
| HC2-80        | GCCTACAGAAAAAAGGTTCTGGGATCTACATGGCAGGGAGGGCTGCACTGACATTGAT |
| HC2B          | -----                                                      |
| HC2C          | -----                                                      |
| HC2D-KIAA1058 | GCCTACAGAAAAAAGGTTCTGGGATCTACATGGCAGGGAGGGCTGCACTGACATTGAT |
| HC2E          | -----                                                      |
| HC2F          | -----                                                      |

|               |                                                               |
|---------------|---------------------------------------------------------------|
| HC2A          | GCCTGGGGGACCTTTTGCCTCGACTCGTGCCGGAAATCTGATCGTAATCAGGGTACAGAA  |
| HC2-80        | GCCTGGGGGACCTTTTGCCTCGACTCGTGCCGGAAATCTGATCGTAATCAGGGTACAGAA  |
| HC2B          | -----                                                         |
| HC2C          | -----                                                         |
| HC2D-KIAA1058 | GCCTGGGGGACCTTTTGCCTCGAGGCTGAGCTGGAAAAATCTTGAAAAATATTTTTT---T |
| HC2E          | -----                                                         |
| HC2F          | -----                                                         |

|               |                                                              |
|---------------|--------------------------------------------------------------|
| HC2A          | CTTACTAGTTTTGTCTAGGAGTATGTTGTATGACTAGGATTTGTGCTATTATCTCATTCA |
| HC2-80        | CTTACTAGTTTTGTCTAGGAGTATGTTGTATGACTAGGATTTGTGCTATTATCTCATTCA |
| HC2B          | -----                                                        |
| HC2C          | -----                                                        |
| HC2D-KIAA1058 | TTTCCTGTGGCACATTCAGGTTGAATACAAGAACTATTTTTGTGACTAGTTTTTGATGAC |
| HC2E          | -----                                                        |
| HC2F          | -----                                                        |

|               |                                                              |
|---------------|--------------------------------------------------------------|
| HC2A          | ACAACATAGAGCAAGAATAGTGAGCTAACTGAGCTAGACACTCAATTAATCCGCTACTGG |
| HC2-80        | ACAACATAGAGCAAGAATAGTGAGCTAACTGAGCTAGACACTCAATTAATCCGCTACTGG |
| HC2B          | -----                                                        |
| HC2C          | -----                                                        |
| HC2D-KIAA1058 | CTAAGGGAACTGACCATTGTAATTTTTGTACCAGTGAACCAGGAGATTTAGTGCTTTTAT |
| HC2E          | -----                                                        |
| HC2F          | -----                                                        |

FIG. 3A (cont.)

|               |                                                               |
|---------------|---------------------------------------------------------------|
| HC2A          | CTTCAAGTCAGAACTTTGTCATTAATCATCGACTCCGGGACGGTCATATATGTATTACAT  |
| HC2-80        | CTTCAAGTCAGAACTTTGTCATTAATCATCGACTCCGGGACGGTCATATATGTATTACAT  |
| HC2B          | -----                                                         |
| HC2C          | -----                                                         |
| HC2D-KIAA1058 | ATTCATTTTCCTTGCATTTAAGAAAATATGAAAGCTTAAGGAATTATGTGAGCTTAAAACT |
| HC2E          | -----                                                         |
| HC2F          | -----                                                         |

|               |                                                               |
|---------------|---------------------------------------------------------------|
| HC2A          | TTCTACATTTTTAATACTCACATGGGCTTATGCATTAAGTTTAATTGTGATAAAATTTGTG |
| HC2-80        | TTCTACATTTTTAATACTCACATGGGCTTATGCATTAAGTTTAATTGTGATAAAATTTGTG |
| HC2B          | -----                                                         |
| HC2C          | -----                                                         |
| HC2D-KIAA1058 | AGTCAAGCAGTTTAGAACCAAAGGCCTATATTAATAACCGCAACTATGCTGAAAAGTACA  |
| HC2E          | -----                                                         |
| HC2F          | -----                                                         |

|               |                                                                |
|---------------|----------------------------------------------------------------|
| HC2A          | CTGGTCCAGTATATGCAATACACTTTAATGGTTTATTCTTGTGCATAAAAAATGTGCAATAT |
| HC2-80        | CTGGTCCAGTATATGCAATACACTTTAATGGTTTATTCTTGTGCATAAAAAATGTGCAATAT |
| HC2B          | -----                                                          |
| HC2C          | -----                                                          |
| HC2D-KIAA1058 | AAGTAGTACAGTATATTGTTATGTACATATCATTGTTAATACAGTCCTGGCATTCTGTAC   |
| HC2E          | -----                                                          |
| HC2F          | -----                                                          |

|               |                                                              |
|---------------|--------------------------------------------------------------|
| HC2A          | GGAGATGTATACAAGTCTTTACT-----                                 |
| HC2-80        | GGAGATGTATACAAGTCTTTACT-----                                 |
| HC2B          | -----                                                        |
| HC2C          | -----                                                        |
| HC2D-KIAA1058 | ATATATGTATTACATTTCTACATTTTTAATACTCACATGGGCTTATGCATTAAGTTTAAT |
| HC2E          | -----                                                        |
| HC2F          | -----                                                        |

|               |                                                              |
|---------------|--------------------------------------------------------------|
| HC2A          | -----                                                        |
| HC2-80        | -----                                                        |
| HC2B          | -----                                                        |
| HC2C          | -----                                                        |
| HC2D-KIAA1058 | TGTGATAAATTTGTGCTGTTCCAGTATATGCAATACACTTTAATGTTTTATTCTTGTACA |
| HC2E          | -----                                                        |
| HC2F          | -----                                                        |

|               |                                                              |
|---------------|--------------------------------------------------------------|
| HC2A          | -----                                                        |
| HC2-80        | -----                                                        |
| HC2B          | -----                                                        |
| HC2C          | -----                                                        |
| HC2D-KIAA1058 | TAAAAATGTGCAATATGGAGATGTATACAGTCTTTACTATATTAGGTTTATAAACAGTTT |
| HC2E          | -----                                                        |
| HC2F          | -----                                                        |

FIG. 3A (cont.)

HC2A  
HC2-80  
HC2B  
HC2C  
HC2D-KIAA1058  
HC2E  
HC2F

HC2A  
HC2-80  
HC2B  
HC2C  
HC2D-KIAA1058  
HC2E  
HC2F

HC2A  
HC2-80  
HC2B  
HC2C  
HC2D-KIAA1058  
HC2E  
HC2F

HC2A  
HC2-80  
HC2B  
HC2C  
HC2D-KIAA1058  
HC2E  
HC2F

FIG. 3A (cont.)

|         |                                                              |
|---------|--------------------------------------------------------------|
| HC2A    | -----                                                        |
| HC2A-80 | -----                                                        |
| HC2B    | -----                                                        |
| HC2C    | -----                                                        |
| HC2D    | ASGNLDKNARFSAIYRQDSNKLSNDDMLKLLADFRKPEKMAKLPVILGNLDITIDNVSSD |
| HC2E    | -----                                                        |
| HC2F    | -----                                                        |

|         |                                                             |
|---------|-------------------------------------------------------------|
| HC2A    | -----                                                       |
| HC2A-80 | -----                                                       |
| HC2B    | -----                                                       |
| HC2C    | -----                                                       |
| HC2D    | FPNYVNSSYIPTKQFETCSKTPITFEVEEFVPCIPKHTQPYTIYTNHLYVYPKYLYDSQ |
| HC2E    | -----                                                       |
| HC2F    | -----                                                       |

|         |                                                               |
|---------|---------------------------------------------------------------|
| HC2A    | -----VLHHHQNPFEFYDEIK                                         |
| HC2A-80 | -----                                                         |
| HC2B    | -----                                                         |
| HC2C    | -----                                                         |
| HC2D    | KSFAKARNIAICIEFKDSDEEDSQPLKCIYGRPGGPVFTRSAFAAVLHHHQNPFEFYDEIK |
| HC2E    | -----                                                         |
| HC2F    | -----                                                         |

|         |                                                              |
|---------|--------------------------------------------------------------|
| HC2A    | IELPTQLHEKHLLLLTFFHVSCDNSSKGSTKKRDVVETQVGYSWLPLLKDGRVVTSEQHI |
| HC2A-80 | -----                                                        |
| HC2B    | -----                                                        |
| HC2C    | -----                                                        |
| HC2D    | IELPTQLHEKHLLLLTFFHVSCDNSSKGSTKKRDVVETQVGYSWLPLLKDGRVVTSEQHI |
| HC2E    | -----                                                        |
| HC2F    | -----                                                        |

|         |                                                             |
|---------|-------------------------------------------------------------|
| HC2A    | PVSANLPSGYLGYQELGMGRHYGPEIKWVDGGKPLLKISTHLVSTVYTQDQHLHNFQYC |
| HC2A-80 | -----                                                       |
| HC2B    | -----                                                       |
| HC2C    | -----                                                       |
| HC2D    | PVSANLPSGYLGYQELGMGRHYGPEIKWVDGGKPLLKISTHLVSTVYTQDQHLHNFQYC |
| HC2E    | -----                                                       |
| HC2F    | -----                                                       |

|         |                                                              |
|---------|--------------------------------------------------------------|
| HC2A    | OKTESGAQALGNELVKYLKSLHAMEGHVMIAFLPTILNQLFRVLTRATQEEVAVNVTRVI |
| HC2A-80 | -----                                                        |
| HC2B    | -----AMEGHVMIAFLPTILNQLFRVLTRATQEEVAVNVTRVI                  |
| HC2C    | -----                                                        |
| HC2D    | OKTESGAQALGNELVKYLKSLHAMEGHVMIAFLPTILNQLFRVLTRATQEEVAVNVTRVI |
| HC2E    | -----AMEGHVMIAFLPTILNQLFRVLTRATQEEVAVNVTRVI                  |
| HC2F    | -----                                                        |



|         |                                                              |
|---------|--------------------------------------------------------------|
| HC2A    | IHVVAQCHEEGLESHLRSYVKYAYKAEPYVASEYKTVHEELTKSMTTILKPSADFLTSNK |
| HC2A-80 | -----                                                        |
| HC2B    | IHVVAQCHEEGLESHLRSYVKYAYKAEPYVASEYKTVHEELTKSMTTILKPSADFLTSNK |
| HC2C    | -----                                                        |
| HC2D    | IHVVAQCHEEGLESHLRSYVKYAYKAEPYVASEYKTVHEELTKSMTTILKPSADFLTSNK |
| HC2E    | IHVVAQCHEEGLESHLRSYVKYAYKAEPYVASEYKTVHEELTKSMTTILKPSADFLTSNK |
| HC2F    | -----                                                        |

|         |                                                                   |
|---------|-------------------------------------------------------------------|
| HC2A    | LLRYSWFFFDVLIK SMAQH LIEN SKVKLLRNQRF PAS YHHAAETVVNMLMPHITQKFGDN |
| HC2A-80 | -----                                                             |
| HC2B    | LLRYSWFFFDVLIK SMAQH LIEN SKVKLLRNQRF PAS YHHAAETVVNMLMPHITQKFGDN |
| HC2C    | -----                                                             |
| HC2D    | LLKYSWFFFDVLIK SMAQH LIEN SKVKLLRNQRF PAS YHHAAETVVNMLMPHITQKFRDN |
| HC2E    | LLRYSWFFFDVLIK SMAQH LIEN SKVKLLRNQRF PAS YHHAAETVVNMLMPHITQKFGDN |
| HC2F    | -----                                                             |

|         |                                                              |
|---------|--------------------------------------------------------------|
| HC2A    | PEASKNANHSLAVFIKRCFTFMDRGFVFKQINNYISCFAPGDPKTLFEYKFEFLRVVCNH |
| HC2A-80 | -----                                                        |
| HC2B    | PEASKNANHSLAVFIKRCFTFMDRGFVFKQINNYISCFAPGDPKTLFEYKFEFLRVVCNH |
| HC2C    | -----                                                        |
| HC2D    | PEASKNANHSLAVFIKRCFTFMDRGFVFKQINNYISCFAPGDPKTLFEYKFEFLRVVCNH |
| HC2E    | PEASKNANHSLAVFIKRCFTFMDRGFVFKQINNYISCFAPGDPKTLFEYKFEFLRVVCNH |
| HC2F    | -----                                                        |

|         |                                                              |
|---------|--------------------------------------------------------------|
| HC2A    | EHYIPLNLPMPFGKGRIQRYQDLQDYSLTDEFCRNHFLVGLLLREVG TALQEFREVRLI |
| HC2A-80 | -----OLDYSLTDEFCRNHFLVGLLLREVG TALQEFREVRLI                  |
| HC2B    | EHYIPLNLPMPFGKGRIQRYQDLQDYSLTDEFCRNHFLVGLLLREVG TALQEFREVRLI |
| HC2C    | -----                                                        |
| HC2D    | EHYIPLNLPMPFGKGRIQRYQDLQDYSLTDEFCRNHFLVGLLLREVG TALQEFREVRLI |
| HC2E    | EHYIPLNLPMPFGKGRIQRYQDLQDYSLTDEFCRNHFLVGLLLREVG TALQEFREVRLI |
| HC2F    | -----                                                        |

|         |                                                              |
|---------|--------------------------------------------------------------|
| HC2A    | AISVLKNLLIKHSFDDRYASRSHQARIATLYLPLFGLLIENVQRINVRDVSPFPVNAGMT |
| HC2A-80 | AISVLKNLLIKHSFDDRYASRSHQARIATLYLPLFGLLIENVQRINVRDVSPFPVNAGMT |
| HC2B    | AISVLKNLLIKHSFDDRYASRSHQARIATLYLPLFGLLIENVQRINVRDVSPFPVNAGMT |
| HC2C    | -----                                                        |
| HC2D    | AISVLKNLLIKHSFDDRYASRSHQARIATLYLPLFGLLIENVQRINVRDVSPFPVNAGMT |
| HC2E    | AISVLKNLLIKHSFDDRYASRSHQARIATLYLPLFGLLIENVQRINVRDVSPFPVNAGMT |
| HC2F    | -----                                                        |

|         |                                                              |
|---------|--------------------------------------------------------------|
| HC2A    | VKDESLALPAVNPLVTPQKGSTLDNSLHKDLLGAISGIASPYTTSTPNINSVRNADSRGS |
| HC2A-80 | VKDESLALPAVNPLVTPQKGSTLDNSLHKDLLGAISGIASPYTTSTPNINSVRNADSRGS |
| HC2B    | VKDESLALPAVNPLVTPQKGSTLDNSLHKDLLGAISGIASPYTTSTPNINSVRNADSRGS |
| HC2C    | -----                                                        |
| HC2D    | VKDESLALPAVNPLVTPQKGSTLDNSLHKDLLGAISGIASPYTTSTPNINSVRNADSRGS |
| HC2E    | VKDESLALPAVNPLVTPQKGSTLDNSLHKDLLGAISGIASPYTTSTPNINSVRNADSRGS |
| HC2F    | -----ADSRGS                                                  |

|         |                                                                 |
|---------|-----------------------------------------------------------------|
| HC2A    | LISTDSGNSLPERNSEKSNSLDKHQSSSTLGNSVVRCDKLDQSEIKSLLMCFLYILKSMS    |
| HC2A-80 | LISTDSGNSLPERNSEKSNSLDKHQSSSTLGNSVVRCDKLDQSEIKSLLMCFLYILKSMS    |
| HC2B    | LISTDSGNSLPERNSEKSNSLDKHQSSSTLGNSVVRCDKLDQSEIKSLLMCFLYILKSMS    |
| HC2C    | -----                                                           |
| HC2D    | LISTDSGNSLPERNSEKSNSLDKHQSSSTLGNSVVRCDKLDQSEIKSLLMCFLYILKSMS    |
| HC2E    | LISTDSGNSLPERNSEKSNSLDKHQSSSTLGNSVVRCDKLDQSEIKSLLMCFLYILKSMS    |
| HC2F    | LISTDSGNSLPERNSEKSNSLDKHQSSSTLGNSVVRCDKLDQSEIKSLLMCFLYILKSMS    |
|         |                                                                 |
| HC2A    | DDALFTYWNKASTSEIMDFFTISEVCLHQFQYMGKRYIARNQOGLGPIVHDRKSQTL PVS   |
| HC2A-80 | DDALFTYWNKASTSEIMDFFTISEVCLHQFQYMGKRYIARNQOGLGPIVHDRKSQTL PVS   |
| HC2B    | DDALFTYWNKASTSEIMDFFTISEVCLHQFQYMGKRYIARNQOGLGPIVHDRKSQTL PVS   |
| HC2C    | -----                                                           |
| HC2D    | DDALFTYWNKASTSEIMDFFTISEVCLHQFQYMGKRYIAR-----                   |
| HC2E    | DDALFTYWNKASTSEIMDFFTISEVCLHQFQYMGKRYIARNQOGLGPIVHDRKSQTL PVS   |
| HC2F    | DDALFTYWNKASTSEIMDFFTISEVCLHQFQYMGKRYIAS-----VR--KISSVLGIS      |
|         |                                                                 |
| HC2A    | RNRTGMMHARLQQLGSLDNSLT FNHSYGHSDADVLHQSLLEANIATEVCLTALDTLSLFT   |
| HC2A-80 | RNRTGMMHARLQQLGSLDNSLT FNHSYGHSDADVLHQSLLEANIATEVCLTALDTLSLFT   |
| HC2B    | RNRTGMMHARLQQLGSLDNSLT FNHSYGHSDADVLHQSLLEANIATEVCLTALDTLSLFT   |
| HC2C    | -----                                                           |
| HC2D    | ---TGMHARLQQLGSLDNSLT FNHSYGHSDADVLHQSLLEANIATEVCLTALDTLSLFT    |
| HC2E    | RNRTGMMHARLQQLGSLDNSLT FNHSYGHSDADVLHQSLLEANIATEVCLTALDTLSLFT   |
| HC2F    | V-----D-NG-----YGHSDADVLHQSLLEANIATEVCLTALDTLSLFT               |
|         |                                                                 |
| HC2A    | LAFKNQLLADHGHNPIMKKVFDVYLCFLQKHQSETALKNVFTALRS LIYKFPSTFYEGRA   |
| HC2A-80 | LAFKNQLLADHGHNPIMKKVFDVYLCFLQKHQSETALKNVFTALRS LIYKFPSTFYEGRA   |
| HC2B    | LAFK--LLADHGHNPIMKKVFDVYLCFLQKHQSETALKNVFTALRS LIYKFPSTFYEGRA   |
| HC2C    | -----                                                           |
| HC2D    | LAFKNQLLADHGHNPIMKKVFDVYLCFLQKHQSETALKNVFTALRS LIYKFPSTFYEGRA   |
| HC2E    | LAFKNQLLADHGHNPIMKKVFDVYLCFLQKHQSETALKNVFTALRS LIYKFPSTFYEGRA   |
| HC2F    | LAFKNQLLADHGHNPIMKKK-----                                       |
|         |                                                                 |
| HC2A    | DMCAALCYEILKCCNSKLSSIRTEASQLLYFLMRNNFDYTGKKS FVRTHLQVIISVSQLI   |
| HC2A-80 | DMCAALCYEILKCCNSKLSSIRTEASQLLYFLMRNNFDYTGKKS FVRTHLQVIISVSQLI   |
| HC2B    | DMCAALCYEILKCCNSKLSSIRTEASQLLYFLMRNNFDYTGKKS FVRTHLQVIISVSQLI   |
| HC2C    | -----                                                           |
| HC2D    | DMCAALCYEILKCCNSKLSSIRTEASQLLYFLMRNNFDYTGKKS FVRTHLQVIISVSQLI   |
| HC2E    | DMCAALCYEILKCCNSKLSSIRTEASQLLYFLMRNNFDYTGKKS FVRTHLQVIISVSQLI   |
| HC2F    | -----                                                           |
|         |                                                                 |
| HC2A    | ADVVGIGETR FQQSLSI INNCANS DRLIKHTSFSSDVKDLTKRIRTVLMATAQMKEHEND |
| HC2A-80 | ADVVGIGETR FQQSLSI INNCANS DRLIKHTSFSSDVKDLTKRIRTVLMATAQMKEHEND |
| HC2B    | ADVVGIGETR FQQSLSI INNCANS DRLIKHTSFSSDVKDLTKRIRTVLMATAQMKEHEND |
| HC2C    | -----                                                           |
| HC2D    | ADVVGIGETR FQQSLSI INNCANS DRLIKHTSFSSDVKDLTKRIRTVLMATAQMKEHEND |
| HC2E    | ADVVGIGETR FQQSLSI INNCANS DRLIKHTSFSSDVKDLTKRIRTVLMATAQMKEHEND |
| HC2F    | -----                                                           |

|         |                                                               |
|---------|---------------------------------------------------------------|
| HC2A    | PEMLVDLQYSLAKSYASTPELRKTWLDSMARIHVKNGBLSEAAMCYVHVLTALVAEYLTRK |
| HC2A-80 | PEMLVDLQYSLAKSYASTPELRKTWLDSMARIHVKNGBLSEAAMCYVHVLTALVAEYLTRK |
| HC2B    | PEMLVDLQYSLAKSYASTPELRKTWLDSMARIHVKNGBLSEAAMCYVHVLTALVAEYLTRK |
| HC2C    | -----                                                         |
| HC2D    | PEMLVDLQYSLAKSYASTPELRKTWLDSMARIHVKNGBLSEAAMCYVHVLTALVAEYLTRK |
| HC2E    | PEMLVDLQYSLAKSYASTPELRKTWLDSMARIHVKNGBLSEAAMCYVHVLTALVAEYLTRK |
| HC2F    | -----                                                         |

|         |                                                            |
|---------|------------------------------------------------------------|
| HC2A    | -----GVFRQGCTAFRVITPNIDEEASMMEDVGMQDVHFNE                  |
| HC2A-80 | -----GVFRQGCTAFRVITPNIDEEASMMEDVGMQDVHFNE                  |
| HC2B    | -----GVFRQGCTAFRVITPNIDEEASMMEDVGMQDVHFNE                  |
| HC2C    | -----FRQGCTAFRVITPNIDEEASMMEDVGMQDVHFNE                    |
| HC2D    | EAVQWEPPLPHSHSACLRRSRGGVFRQGCTAFRVITPNIDEEASMMEDVGMQDVHFNE |
| HC2E    | -----GVFRQGCTAFRVITPNIDEEASMMEDVG-----                     |
| HC2F    | -----                                                      |

|         |                                                        |
|---------|--------------------------------------------------------|
| HC2A    | DVLMELLEQCADGLWKAERYELIADYKLIPIYKRR-----               |
| HC2A-80 | DVLMELLEQCADGLWKAERYELIADYKLIPIYKRR-----               |
| HC2B    | DVLMELLEQCADGLWKAERYELIADYKLIPIYKRRDFFERLAHLYDTLHRAYSK |
| HC2C    | DVLMELLEQCADGLWKAERYELIADYKLIPIYKRRDFFERLAHLYDTLHRAYSK |
| HC2D    | DVLMELLEQCADGLWKAERYELIADYKLIPIYKRRDFFERLAHLYDTLHRAYSK |
| HC2E    | -----KAERYELIADYKLIPIYKRRDFFERLAHLYDTLHRAYSK           |
| HC2F    | -----                                                  |

|         |                                                             |
|---------|-------------------------------------------------------------|
| HC2A    | -----DFFEDEDGKEYIYKEPKLTPLSE                                |
| HC2A-80 | -----DFFEDEDGKEYIYKEPKLTPLSE                                |
| HC2B    | VTEVMHSGRRLLGTYFRVAFFGQ-----GFFEDEDGKEYIYKEPKLTPLSE         |
| HC2C    | VTEVMHSGRRLLGTYFRVAFFGQ-----GFFEDEDGKEYIYKEPKLTPLSE         |
| HC2D    | VTEVMHSGRRLLGTYFRVAFFGQAQYQFTDSETDVEGFFEDEDGKEYIYKEPKLTPLSE |
| HC2E    | VTEVMHSGRRLLGTYFRVAFFGQ-----GFFEDEDGKEYIYKEPKLTPLSE         |
| HC2F    | -----                                                       |

|         |                                                             |
|---------|-------------------------------------------------------------|
| HC2A    | ISQRLKLYSDKFGSENVKMIQDSGKVNPKDLDSKYAYIQVTHVIPFFDEKELQERKTEF |
| HC2A-80 | ISQRLKLYSDKFGSENVKMIQDSGKVNPKDLDSKYAYIQVTHVIPFFDEKELQERKTEF |
| HC2B    | ISQRLKLYSDKFGSENVKMIQDSGKVNPKDLDSKYAYIQVTHVIPFFDEKELQERKTEF |
| HC2C    | ISQRLKLYSDKFGSENVKMTQDSGKVNPKDLDSKYAYIQVTHVIPFFDEKELQERKTEF |
| HC2D    | ISQRLKLYSDKFGSENVKMIQDSGKVNPKDLDSKYAYIQVTHVIPFFDEKELQERKTEF |
| HC2E    | ISQRLKLYSDKFGSENVKMIQDSGKVNPKDLDSKYAYIQVTHVIPFFDEKELQERKTEF |
| HC2F    | -----                                                       |

|         |                                                              |
|---------|--------------------------------------------------------------|
| HC2A    | ERSHNIRRFMFEMPFTQTGKRQGGVEEQCKRRTILTAIHCFPYVKKRIPVMYQHHTDLNP |
| HC2A-80 | ERSHNIRRFMFEMPFTQTGKRQGGVEEQCKRRTILTAIHCFPYVKKRIPVMYQHHTDLNP |
| HC2B    | ERSHNIRRFMFEMPFTQTGKRQGGVEEQCKRRTILTAIHCFPYVKKRIPVMYQHHTDLNP |
| HC2C    | ERSHNIRRFMFEMPFTQTGKRQGGVEEQCKRRTILTAIHCFPYVKKRIPVMYQHHTDLNP |
| HC2D    | ERSHNIRRFMFEMPFTQTGKRQGGVEEQCKRRTILTAIHCFPYVKKRIPVMYQHHTDLNP |
| HC2E    | ERSHNIRRFMFEMPFTQTGKRQGGVEEQCKRRTILTAIHCFPYVKKRIPVMYQHHTDLNP |
| HC2F    | -----                                                        |





~ 7.5 kb —

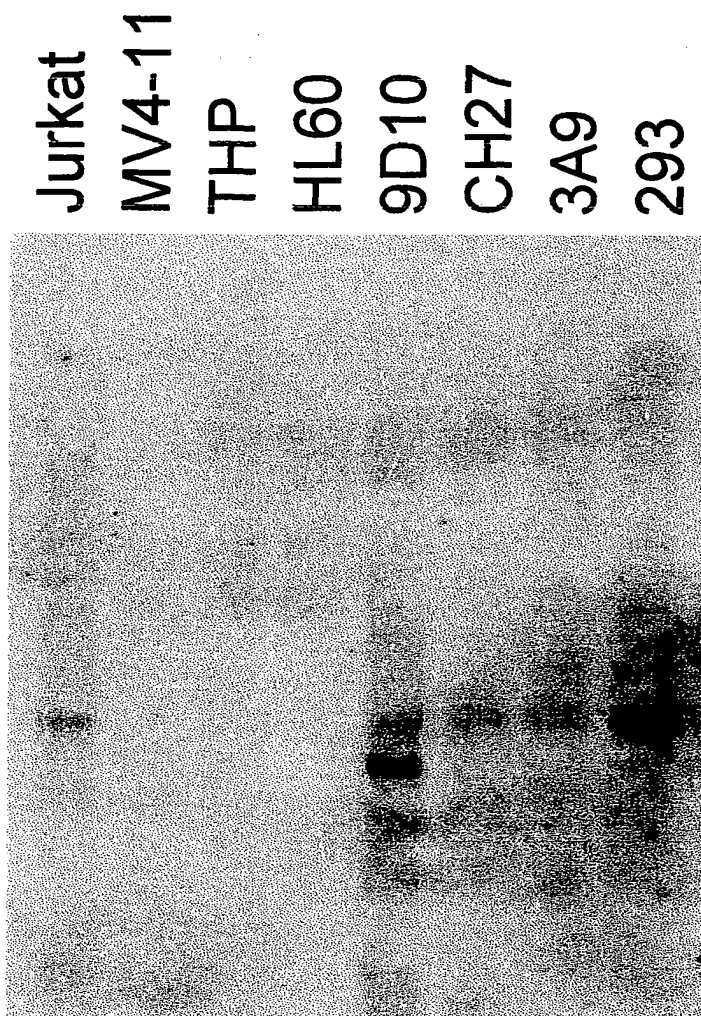


Fig. 4B

|      |                                                               |
|------|---------------------------------------------------------------|
| HC2A | -----                                                         |
| KIAA | ASGNLDKNARFS AIYRQDSNKLSNDDMLKLLADFRKPEKMAKLPVILGNLDITIDNVSSD |
| rat  | -----                                                         |
| HC4  | -----                                                         |
| HC1  | -----                                                         |
| HC3  | -----                                                         |
| HC5  | -----                                                         |

|      |                                                              |
|------|--------------------------------------------------------------|
| HC2A | -----                                                        |
| KIAA | FPNYVNSSYIPTKQFETCSKTPITFEVEEFVPCIPKHTQPYTIYTNHLYVYPKYLKYDSQ |
| rat  | -----                                                        |
| HC4  | -----                                                        |
| HC1  | -----                                                        |
| HC3  | -----                                                        |
| HC5  | -----                                                        |

|      |                                                               |
|------|---------------------------------------------------------------|
| HC2A | -----VLHHHQNPFEFYDEIK                                         |
| KIAA | KSFAKARNIAICIEFKDSDEEDSQPLKCIYGRPGGPVFTRSAFAAVLHHHQNPFEFYDEIK |
| rat  | -----                                                         |
| HC4  | -----                                                         |
| HC1  | -----                                                         |
| HC3  | -----                                                         |
| HC5  | -----                                                         |

|      |                                                             |
|------|-------------------------------------------------------------|
| HC2A | -----                                                       |
| KIAA | IELPTQLHEKHLLLTFFHVSCDNSSKGSTKKRDVVETQVGYSWLPLLKDGRVVTSEQHI |
| rat  | IELPTQLHEKHLLLTFFHVSCDNSSKGSTKKRDVVETQVGYSWLPLLKDGRVVTSEQHI |
| HC4  | -----                                                       |
| HC1  | -----                                                       |
| HC3  | -----                                                       |
| HC5  | -----                                                       |

|      |                                                              |
|------|--------------------------------------------------------------|
| HC2A | -----                                                        |
| KIAA | PVSANLPSGYLGYQELGMGRHYGPEIKWVDGGKPLLKISTHLVSTVYTQDQHLHNFFQYC |
| rat  | PVSANLPSGYLGYQELGMGRHYGPEIKWVDGGKPLLKISTHLVSTVYTQDQHLHNFFQYC |
| HC4  | -----                                                        |
| HC1  | -----                                                        |
| HC3  | -----GPGPARSTVSISLISNSARV                                    |
| HC5  | -----                                                        |

|      |                                                              |
|------|--------------------------------------------------------------|
| HC2A | -----                                                        |
| KIAA | QKTESGAQALGNELVKYLKSLHAMEGHVMIAFLPTILNQLFRVLT-RATQEEVAVNVTRV |
| rat  | QKTESGAQALGNELVKYLKSLHAMEGHVMIAFLPTILNQLFRVLT-RATQEEVAVNVTRV |
| HC4  | -----MEIQVLIRFLSVILMQLFWVLPNMIHEDDVPISCPMV                   |
| HC1  | -----MSFLPIILNQLFKVLV-QNEEDEITTTVTRV                         |
| HC3  | NRSRSLSNSNPDISGTPTSPDDEVRSIIGSKGLDRSNSWVNTGGPKAAPWGSNPSPSAES |
| HC5  | -----                                                        |

Fig. 5A

HC2A I IHVVAQCHEE SHLRSYVKYAYKAEPYVASEYKTVHEEL T TILKPSADFLTSN  
 KIAA I IHVVAQCHEE SHLRSYVKYAYKAEPYVASEYKTVHEEL T TILKPSADFLTSN  
 rat -----  
 HC4 LFHIVSKCHEEGLDSYLSSFIKYSFRPGKPSAPQAPLIHETLATMMIALLKQSADFLAIN  
 HC1 LPDIVAKCHEEQLDHSVQSYIKFVFKTR---ACKERPVEDLAKNVTGLLK-SNDSPTVK  
 HC3 TQAMDRSCNRMSSHTETSSFLQTLTGRLP----TKKLFHEELALQWVVCSG--SVR---E  
 HC5 -----

Cadherin  
 Cleavage

HC2A KLLRYSWFFFVDVLIKSMAQHLENSKVLLRNQRFPAHYHAAETVVNMLMPHITQKFGD  
 KIAA KLLKYSWFFFVDVLIKSMAQHLENSKVLLRNQRFPAHYHAAETVVNMLMPHITQKFRD  
 rat -----  
 HC4 KLLKYSWFFFEEIIAKSMATYLLEENKIKLTHGQRFPAHYHAAETVVNMLMPHITQKFGD  
 HC1 HVLKHSWFFFFAIILKSMAQHLEIDTNKIQLPRPQRFPAHYHAAETVVNMLMPHITQKFRD  
 HC3 SALQQAWFFFELMVKSMVHLLYFNDKLEAPRKSRRFERFMDIAALVSTIASDIVSRFQK  
 HC5 -----

HC2A NPEASKNANHSLAVFIKRCFTFMDRGFVFKQIN---NYIS--CFAPGDPKTLFEYKFEFL  
 KIAA NPEASKNANHSLAVFIKRCFTFMDRGFVFKQIN---NYIS--CFAPGDPKTLFEYKFEFL  
 rat -----  
 HC4 IPKESRNVNYSLASFLKCCLTLMDRGFVFNLIN---DYIS--GFSPKDPKVLAEYKFEFL  
 HC1 ALEETRATHSVARFLKRCFTFMDRGCVFKMVN---NYIS--MFSSGDLKTLQYKFEFL  
 HC3 DTEMVERLNTSLAFFLNDLLSVMDRGFVFLSLIKSCYQVSSKLYSLPNPSVLVSLRLDFL  
 HC5 -----

HC2A RVVCNHEHYIPLNLPM-----PFGKGRIQR-----YQDLQL---DYSLTDEF  
 KIAA RVVCNHEHYIPLNLPM-----PFGKGRIQR-----YQDLQL---DYSLTDEF  
 rat -----  
 HC4 QTICNHEHYIPLNLPM-----AFAKPKLQR-----VQDSNL---EYSLSDEY  
 HC1 QEVCQHEHFIPCLPIRSANIPDPLTPSES-----TQELHASDMPEYSVTNEF  
 HC3 RIICSHEHYVTNLNPLCSLLTPPASPSVSSATSQSSGFSTNVQDQKIANMFELS--VPF  
 HC5 -----MNADTAPTSPCPSIS---SQNSSSCSSFQDQKIASMFDRTSRVPA

HC2A CRNHFLVGLLLREVGTALQEFRE----VRLIAISVLKNLLIKHSFDDRYASRSHQARIAT  
 KIAA CRNHFLVGLLLREVGTALQEFRE----VRLIAISVLKNLLIKHSFDDRYASRSHQARIAT  
 rat -----  
 HC4 CKHHFLVGLLLRETSIALQDNYE----IRYTAISVIKNLLIKHAFDTRYQHKNQQAQIAQ  
 HC1 CRKHFLIGILLREVGFALQEDQD----VRHLALAVLKNLMKHSFDDRYREPRKQAQIAS  
 HC3 RQOQHYLAGLVLTELAVILDPAEGLFGLHKKVINMVHNLSSHDSDPYSDPQIKARVAM  
 HC5 SSTS-SPGLLFTELAALDAEGEGISEVQORKAVSAIHSLLSSHDLDPKVCVKEVKVIAA

HC2A LYLPLFGLLIENVQORINVRDVSPFPVNAG-MTVKDESALPAVNPLVTPQKGSTLDNSLH  
 KIAA LYLPLFGLLIENVQORINVRDVSPFPVNAG-MTVKDESALPAVNPLVTPQKGSTLDNSLH  
 rat -----  
 HC4 LYLPLFVGLLLENIQRLAGRDTLYSCAMPNSASRDEFPCG-----FTSP--AN--RGSLS  
 HC1 LYMPLYGMLLDNMPRIYLDLYPFTVNTSNQGSRDDLSNNGGFQSQTAIKHANSVDTSFS  
 HC3 LYLPLIGIIMETVPQLYDFTETHNQRGRPICATDDYESE-----SG---SMIS  
 HC5 LYLPLVGIILDALPQLCDFTVADTRRYR---TSGSDEEQE-----GA---GAIT

HC2A KDLLGAISGIASPYTTSTPNINSVRNADSRGSLISTDSGNSLPERNSEKSNSLDKHQSS  
 KIAA KDLLGAISGIASPYTTSTPNINSVRNADSRGSLISTDSGNSLPERNSEKSNSLDKHQSS  
 rat -----  
 HC4 TDKDTAYGSFQNG-----HGKREDRSLIP-EGATGFPDQNGTGEN-----TRQS  
 HC1 KDVLNSIAAFSS-----IAISTVNHADSRASLASLDNPNSTNEKSSEKTDNCEKIPRPL  
 HC3 QTVAMAIAGTSVPQ-----LTRPGSFLLTSTSGRQHT-----  
 HC5 QNALAIAGNNFN-----LKTSG-IVLSSSLPYKQYN-----

Fig. 5A (cont.)



|      |                                                                |
|------|----------------------------------------------------------------|
| HC2A | TLGNSVVRCDKLDQSEIKSLLMCFLYILKMSDDALFTYWN-KASTSELMDFFTISEVCL    |
| KIAA | TLGNSVVRCDKLDQSEIKSLLMCFLYILKMSDDALFTYWN-KASTSELMDFFTISEVCL    |
| rat  | -----                                                          |
| HC4  | STRSSVSQYNRLDQYEIRSLLMCYLYIVKMISEDTLTYWN-KVSPQELINILILLEVCL    |
| HC1  | ALIGSTLRFDRLDQAETRSLLMCFLHIMKTISYETLIAYWQ-RAPSPEVSDFFSILDVCL   |
| HC3  | -----TFSAESSRSLICLLWVLKN-ADETVLQKWFTDLSVLQNLRLDLLLYLCV         |
| HC5  | -----MLNADTTRNLMICFLWIMKN-ADQSLIRKWIADLPSTQLNRILDLLFICV        |
|      |                                                                |
| HC2A | HQFOYMGKRYIARNQEGLG--PIVHDRKS-----QTLPVSRNRTGMM                |
| KIAA | HQFOYMGKRYIAR-----TGMM                                         |
| rat  | -----                                                          |
| HC4  | FHFYRMGKRNIARVHDAWLSKHFGIDRKS-----QTMPALRNRSQVM                |
| HC1  | QNFYRLGKRNIIRKIAAAF--KFVQSTQNGTLKGSNPSCQTSGLLAQWMHSTSRHEGHK    |
| HC3  | SCFEYKGGKVFERMNSLTFK--KSKDMRAK-----LEEAILGSGARQEMV             |
| HC5  | LCFEYKGGKQSSDKVSTQVLQ--KSRDVKAR-----LEEALLRGEARGEMV            |
|      |                                                                |
| HC2A | HARLQQL-----GSLDNS-----LTFNHSYGHSDADVLHQSLLEANIATEVC           |
| KIAA | HARLQQL-----GSLDNS-----LTFNHSYGHSDADVLHQSLLEANIATEVC           |
| rat  | -----                                                          |
| HC4  | QARLQHL-----SSLESS-----FTLNHSSTTEADI FHQALLEGNTATEVS           |
| HC1  | QHRSQTLPIIRGK---NALSNPKL----LQMLDNTMTSNSNEIDIVHHVDTEANIATEGC   |
| HC3  | RRSRGQLERSPSGSAFGSQENLRWRKDMTHWRQNTKLDKSRAEIEHEALIDGNLATEAN    |
| HC5  | RRRAPGNDRFP-----GLNENLRWKKEQTHWRQANEKLDKTKAELDQEALISGNLATEAH   |
|      |                                                                |
| HC2A | LTALDTLSLFTLAFKNQLLADHGHNPIMKKVFDVYLCFLQKHQSETALKNVFTALRSLIY   |
| KIAA | LTALDTLSLFTLAFKNQLLADHGHNPIMKKVFDVYLCFLQKHQSETALKNVFTALRSLIY   |
| rat  | -----KLSRGHSPIMKKVFDVYLCFLQKHQSEMAKKNVFTALRSLIY                |
| HC4  | LTVLDTISFFTQCFKTHFLNNDGHNPIMKKVFDIHLAFLKNGQSEVSLKHVFASLRAFIS   |
| HC1  | LTILDVLSLFTQTHQRLQCCDCQNSIMKRGFDTYMLFFQVNSATALKHVFASLRLEFVC    |
| HC3  | LIILDTLEIVVQTVS--VTES--KESILGGVLKVLHSMACNQSAYVLQHC FATQRALVS   |
| HC5  | LIILDMQENIQASS--ALDC--KDSLGGVLRVLVNSLNCQSTTYLTHCFATLRALIA      |
|      |                                                                |
| HC2A | KFPSTFYEGRA DMCAALCYEILKCCNSKLSSIRTEASQLLYFLMRNNFDYTGKKS FVRTH |
| KIAA | KFPSTFYEGRA DMCAALCYEILKCCNSKLSSIRTEASQLLYFLMRNNFDYTGKKS FVRTH |
| rat  | KFPSTFYEGRA DMCAALCYEVLKCCNSKLSSIRTEASQLLYFLMRNNFDYTGKKS FVRTH |
| HC4  | KFPSAFFKGRVNMCAAFCEYVLKCCCTSKI STRNEASALLYLLMRNNFEYTKRKTFLRTH  |
| HC1  | KFPSAFFQGPADLCGSFCYEVKCCNHRSRSTQTEASALLYLFMRKNFEFNKQKSIVRSH    |
| HC3  | KFPELLFEEETEQCADLCRLRLRHCCSSIGTIRSHPSASLYLLMRQNF EIGN--NFARVK  |
| HC5  | KFGDLLFEEVEQCFDLCHQVLHHCSSMDVTRSQACATLYLLMRFSFGATS--NFARVK     |
|      |                                                                |
| HC2A | LQVIISVSQLIADVVGIGETRFOQSLSIINNCANS DRLIKHTSFSSDVKDLTKRIRTVLM  |
| KIAA | LQVIISVSQLIADVVGIGETRFOQSLSIINNCANS DRLIKHTSFSSDVKDLTKRIRTVLM  |
| rat  | LQVIISLSQLIADVVGIGETRFOQSLSIINNCANS DRLIKHTSFSSDVKDLTKRIRTVLM  |
| HC4  | LQIIIAVSQLIADVALSGGSRFQESLFIINNFANS DRPMLARAFPAEVKDLTKRIRTVLM  |
| HC1  | LQLIKAVSQLIAD-AGIGGSRFQHSLAITNNFANGDKQMKNSNFP AEVKDLTKRIRTVLM  |
| HC3  | MOVPMSSLSSLVGTSQNFNEEFLRRSLKTI LTYAEEDLELRETTFPDQVQDLVFNLMILS  |
| HC5  | MOVMSLASLVGRAPDFNEEHLRRSLRTILAYSEEDTAMQMT PPTQVEELLCNLNSILY    |

FIG. 5A (cont.)

|      |                                                                |
|------|----------------------------------------------------------------|
| HC2A | ATAQMKEHENDPEMLVDLQYSLAKSYASTPELRKRWLDSMARIHVKNGDLSEAAMCYVHV   |
| KIAA | ATAQMKEHENDPEMLVDLQYSLAKSYASTPELRKRWLDSMARIHVKNGDLSEAAMCYVHV   |
| rat  | ATAQMKEHENDPEMLVDLQYSLAKSYASTPELRKRWLDSMARIHVKNGDLSEAAMCYVHV   |
| HC4  | ATAQMKEHEKDPPEMLIDLQYSLAKSYASTPELRKRWLDSMAKIHVKNGDLSEAAMCYVHV  |
| HC1  | ATAQMKEHEKDPPEMLVDLQYSLANSYASTPELRRTWLLESMAKIHARNGDLSEAAMCYIHI |
| HC3  | DTVKMKEHQEDPEMLIDLMYRIAKGYQTSPDLRLTLWLQNMAKGHSERSNHAEEAQCLVHS  |
| HC5  | DTVKMREFQEDPEMLMDLMYRIAKSYQASPDRLTLWLQNMAEKHTKKKCYTEAAMCLVHA   |

|      |          |                                                      |                                         |
|------|----------|------------------------------------------------------|-----------------------------------------|
|      |          | SH3                                                  |                                         |
| HC2A | TALVAEYI | TRKGV-----                                           | FRQGCTAFRVITPN                          |
| KIAA | TALVAEYI | TRKEA-----                                           | VQWEPPLPHSHSACLRRSRGGVFRQGCTAFRVITPN    |
| rat  | TALVAEYI | TRKEAD-----                                          | LALQREPPVFPYSHTSCQRKSRGGMFRQGCTAFRVITPN |
| HC4  | AALVAEFI | HRKKL-----                                           | FPNGCSAFKKITPN                          |
| HC1  | AALIAEYI | KRKGWYKVEKICTASLLSEDPHPCDSNSLLTTPSGGSMFSGMWPAFLSITPN |                                         |
| HC3  | AALVAEYI | SMLD-----                                            | RKYLPGVCVTFQNISSN                       |
| HC5  | AALVAEYI | SMLD-----                                            | HSYLPVGSVVSFQNISSN                      |

|      |                                                              |                                        |
|------|--------------------------------------------------------------|----------------------------------------|
| HC2A | IDEEASMMEDVGMQD-----                                         | VHFNEDVLMELLEQCADGLWKAERYELIADIYKLIPI  |
| KIAA | IDEEASMMEDVGMQD-----                                         | VHFNEDVLMELLEQCADGLWKAERYELIADIYKLIPI  |
| rat  | IDEEASMMEDVGMQD-----                                         | VHFNEDVLMELLEQCADGLWKAERLRAGLLTSINSSSP |
| HC4  | IDEEGAMKEDAGMMD-----                                         | VHYSEEVLLLELLEQCVNGLWKAERYEIISEISKLIPI |
| HC1  | IKEEGAAKEDSGMHD-----                                         | TPYNENILVEQLYMCGEFLWKSEERYELIADVNPPIAV |
| HC3  | VLEESAVSDDVVPDEEGICSGKYFTESGLVGLLEQAAASFMSAGMYEAVNEVYKVLPI   |                                        |
| HC5  | VLEESVSVSEDTLSPDEDGVCAGQYFTESGLVGLLEQAAELFSTGGLYETVNEVYKVLPI |                                        |

|      |                                            |                     |            |         |                |        |      |
|------|--------------------------------------------|---------------------|------------|---------|----------------|--------|------|
|      |                                            | ITAM                | ITAM       |         | ITAM           |        | ITAM |
| HC2A | YEKRRD-----                                |                     |            |         |                |        |      |
| KIAA | YEKRRD                                     | FERLAHLYDTLHRAYSKVT | EVMSHGRRL  | LGTYFRV | AFFGQAAQYQFTD  | SETDVE |      |
| rat  | SMKSGGT                                    | LETTHLYDTLHRPYSKVT  | EVITR----- | A-----  | AGSWDLLPGGLFGQ |        |      |
| HC4  | YENRREFENLTQVYRTLHGAYTKILEVMHTKKRLLG-----  |                     |            |         | TFFRVAFYGO     |        |      |
| HC1  | FEKQRDFKKLSDIYYDIHRSYLVKVAEVDNSEKRLFG----- |                     |            |         | RYRVAFYGO      |        |      |
| HC3  | HEANRDAKKLSTIHGKLQEAFSKIVHQSTGWERMFG-----  |                     |            |         | TYFRVGFYG-     |        |      |
| HC5  | LEAHREFRKLTLTHSKLQRAFD                     | SIYNKDH--           | KRMFG----- |         | TYFRVGFYG-     |        |      |

|      |                                                           |               |  |      |
|------|-----------------------------------------------------------|---------------|--|------|
|      |                                                           | ITAM          |  | ITAM |
| HC2A | -FFEDDGKEYIYKEPKLTPLSEISQRLKLYSDKFGSENVKMIQDSGKVNPKDLD    | SKYA          |  |      |
| KIAA | GFFEDEDGKEYIYKEPKLTPLSEISQRLKLYSDKFGSENVKMIQDSGKVNPKDLD   | SKYA          |  |      |
| rat  | GFFEDEDGKEYIYKEPKLTPLSEISQRLKLYSDKFGSENVKMIQDSGKVNPKDLD   | SKFA          |  |      |
| HC4  | SFFEEEDGKEYIYKEPKLTGLSEISLRVLKLYGEKFGTENVKIIQSDKVNKELDP   | KYA           |  |      |
| HC1  | GFFEEEGKEYIYKEPKLTGLSEISQRLKLYADKFGADNVKIIQDSNVKVNPKDLD   | PKYA          |  |      |
| HC3  | TKFGDLDEQEFVYKEFAITKLAEISHRLEGFYGERFGEDEVVEVIKDSNPVDKCKLD | PNKA          |  |      |
| HC5  | SKFGDLDEQEFVYKEFAITKLPEISHRLEAFYGOQFGAEFVEVIKDS           | TPVDKTKLDPNKA |  |      |

|      |                                                              |
|------|--------------------------------------------------------------|
|      | ITAM                                                         |
| HC2A | YIQVTHVIPFFDEKELQERKTEFERSHNIRRFMFEMPFTQTGKRQGGVEEQCKRRTILTA |
| KIAA | YIQVTHVIPFFDEKELQERKTEFERSHNIRRFMFEMPFTQTGKRQGGVEEQCKRRTILTA |
| rat  | YIQVTHVIPFFDEKELQERKTEFERNIRRFMFEMPFTQTGKRQGGVEEQCKRRTILTA   |
| HC4  | HIQVTVKPYFDDKELTERKTEFERNHNISRFEAPYTLGKKQGCIEEQCKRRTILT      |
| HC1  | YIQVTVYVTPFFEEKEIEDRKTDFFEMHNNIRRFVETPFTLSGKKHGGVAEQCKRRTILT |
| HC3  | YIQITVVEPYFDTYEMKDRITYFDKNYNLRRFMYCTPFTLDGRAHGELEHQFRKTILT   |
| HC5  | YIQITVVEPYFDEYEMKDRVITYFEKNFNLRRFMYTTPFTLEGRPRGELHEQYRRNTVLT |

FIG. 5A (cont.)

## Coiled-Coil

HC2A IHCFFPYVKKRIPVVMYQHHTDINPIEVAIDEMSKKVAELRQLCSSAEVDMIKLQKLOGSV  
 KIAA IHCFFPYVKKRIPVVMYQHHTDINPIEVAIDEMSKKVAELRQLCSSAEVDMIKLQKLOGSV  
 rat IHCFFPYVKKRIPVVMYQHHTDINPIEVAIDEMSKKVAELHQLCSSAEVDMIKLQKLOGSV  
 HC4 SNSFFPYVKKRIPINCEQQINIKPIDGATDEIKDKTAELQKLCSSSTDVDMIQLOLQKLOGWV  
 HC1 SHLFFPYVKKRIQVISQSSTEINPIEVAIDEMSRKVSELNQLCTMEEVDMISLOLQKLOGSV  
 HC3 SHAFPPYIKTRVNVTHKEEIIITPIEVAIEDMQKKTQELAFATHQDPADPKMLOMVLQGSV  
 HC5 MHAFPPYIKTRISVIQKEEFVITPIEVAIEDMKKKTLOLAVAINQEPDAKMLQOMVLQGSV

## Coiled-Coil 2

HC2A SVQVNAGPLAYARAFLLDDTNTKRYPDNKVKLLKEVFRQFVEACGQAI~~AVNERLIKEDQLE~~  
 KIAA SVQVNAGPLAYARAFLLDDTNTKRYPDNKVKLLKEVFRQFVEACGQAI~~AVNERLIKEDQLE~~  
 rat SVQVNAGPLAYARAFLLDDTNTKRYPDNKVKLLKEVFRQFVEACGQAI~~AVNERLIKEDQLE~~  
 HC4 SVQVNAGPLAYARAFLLNDSQASKYPKKVSELKDMFRKFIQACSI~~AVNERLIKEDQVE~~  
 HC1 SVKVNAGPMAYARAFLEETNAKKYPDNQVKLLKEIFRQFADACGQAI~~AVNERLIKEDQLE~~  
 HC3 GTTVNQGPLEVAQVFLSEIPSDPKLFRHHNKLRLCFKDFTKRCEDAI~~RKNKSLIGPVQKE~~  
 HC5 GATVNQGPLEVAQVFLAEIPADPKLYRHHNKLRLCFKEFIMRCGEA~~VEKNKRLITADQRE~~

## Coiled-Coil 2

HC2A YQEEMKANYREMAKELSEIMHEQICPLEEKTS-VLPNSLHIFNAISGTPTSTMVHGMTSS  
 KIAA YQEEMKANYREMAKELSEIMHEQLG-----  
 rat YQEEMKANYREIRKELSDIIVERICPGEDKRATKFFPAHLQRHQRTDNKHSGSRVDQFELS  
 HC4 YHEGLKSNFRDMVKELSDIIEHQILQEDTMHSPWMSNTLHVFC~~IAISGTSSDRGYGSPRYA~~  
 HC1 YQEELRSHYKMDLSELSTVMNEQITGRDDLK---RGVDQCTCRVISKATPALPTVSISS  
 HC3 YQRELG---KLSS-----PZ-----  
 HC5 YQELKKNYNKLKENLRPMIEKIPELYKPIFRVESQKRDSFHRSSFRCETQLSQGSZ-

## PBM

HC2A ~~SSVVZ~~-----  
 KIAA -----  
 rat CVTLPHPEPHVGTCFVMCKLRTTFRANHWFCQAQEEAMNGREKEPWTVI~~FNSRFYRSWGK~~  
 HC4 ~~EVZ~~-----  
 HC1 ~~SAEVZ~~-----  
 HC3 -----  
 HC5 -----

HC2A -----  
 KIAA -----  
 rat VHIFV  
 HC4 -----  
 HC1 -----  
 HC3 -----  
 HC5 -----



## CLASP/DOCK MOTIF

|           | F |   |   |   |   | G |   |   |   |   |
|-----------|---|---|---|---|---|---|---|---|---|---|
| CLASP-1   | S | L | L | K | L | G | S | V | S | V |
| TRG       | K | L | L | K | L | G | S | V | S | V |
| KIAA1058  | K | L | L | K | L | G | S | V | S | V |
| CLASP-2   | K | L | L | K | L | G | S | V | S | V |
| CLASP-6   | K | L | L | K | L | G | S | V | S | V |
| CLASP-3   | M | L | Q | M | V | L | Q | G | S | V |
| CLASP-4   | Q | L | L | K | L | G | S | V | S | V |
| CLASP-5   | M | L | Q | M | V | L | Q | G | S | V |
| KIAA0716  | P | L | T | M | C | L | N | G | I | V |
| DOCK2     | P | L | S | M | L | L | N | G | I | V |
| DOCK3     | L | L | S | M | C | L | N | G | I | V |
| DOCK180   | P | L | S | M | L | L | N | G | I | V |
| CONSENSUS | L | M | L | G | V | V | N | G | Y | A |
|           | L |   | I |   |   | V | V | F | + | + |

DOCK2=KIAA0209

DOCK3=KIAA0299

CLASP2variant=KIAA1058

FIG. 5B (cont.)

2 32  
GTT TTA CAC CAT CAC CAA AAC CCA GAA TTT TAT GAT GAG ATT AAA ATA GAG TTG CCC ACT  
val leu his his his gln asn pro glu phe tyr asp glu ile lys ile glu leu pro thr

62 92  
CAG CTG CAT GAA AAG CAC CAC CTG TTG CTC ACA TTC TTC CAT GTC AGC TGT GAC AAC TCA  
gln leu his glu lys his his leu leu leu thr phe phe his val ser cys asp asn ser

122 152  
AGT AAA GGA AGC ACG AAG AAG AGG GAT GTC GTT GAA ACC CAA GTT GGC TAC TCC TGG CTT  
ser lys gly ser thr lys lys arg asp val val glu thr gln val gly tyr ser trp leu

182 212  
CCC CTC CTG AAA GAC GGA AGG GTG GTG ACA AGC GAG CAG CAC ATC CCG GTC TCG GCG AAC  
pro leu leu lys asp gly arg val val thr ser glu gln his ile pro val ser ala asn

242 272  
CTT CCT TCG GGC TAT CTT GGC TAC CAA GAG CTT GGG ATG GGC AGG CAT TAT GGT CCG GAA  
leu pro ser gly tyr leu gly tyr gln glu leu gly met gly arg his tyr gly pro glu

302 332  
ATT AAA TGG GTA GAT GGA GGC AAG CCA CTG CTG AAA ATT TCC ACT CAT CTG GTT TCT ACA  
ile lys trp val asp gly gly lys pro leu leu lys ile ser thr his leu val ser thr  
ref 1.1, 1.2 and 1.3

362 392  
GTG TAT ACT CAG GAT CAG CAT TTA CAT AAT TTT TTC CAG TAC TGT CAG AAA ACC GAA TCT  
val tyr thr gln asp gln his leu his asn phe phe gln tyr cys gln lys thr glu ser

422 452  
GGA GCC CAA GCC TTA GGA AAC GAA CTT GTA AAG TAC CTT AAG AGT CTG CAT GCG ATG GAA  
gly ala gln ala leu gly asn glu leu val lys tyr leu lys ser leu his ala met glu

482 512  
GGC CAC GTG ATG ATC GCC TTC TTG CCC ACT ATC CTA AAC CAG CTG TTC CGA GTC CTC ACC  
gly his val met ile ala phe leu pro thr ile leu asn gln leu phe arg val leu thr

542 572  
AGA GCC ACA CAG GAA GAA GTC GCG GTT AAC GTG ACT CGG GTC ATT ATT CAT GTG GTT GCC  
arg ala thr gln glu glu val ala val asn val thr arg val ile ile his val val ala

602 632  
CAG TGC CAT GAG GAA GGA TTG GAG AGC CAC TTG AGG TCA TAT GTT AAG TAC GCG TAT AAG  
gln cys his glu glu gly leu glu ser his leu arg ser tyr val lys tyr ala tyr lys

662 692  
GCT GAG CCA TAT GTT GCC TCT GAA TAC AAG ACA GTG CAT GAA GAA CTG ACC AAA TCC ATG  
ala glu pro tyr val ala ser glu tyr lys thr val his glu glu leu thr lys ser met

FIG. 4A



CTG GCT CTA CCA GCT GTG AAT CCG CTG GTG ACG CCG CAG AAG GGA AGC ACC CTG GAC AAC  
 leu ala leu pro ala val asn pro leu val thr pro gln lys gly ser thr leu asp asn  
 ref 4.1 and 4.2

1562 1592  
 AGC CTG CAC AAG GAC CTG CTG GGC GCC ATC TCC GGC ATT GCT TCT CCA TAT ACA ACC TCA  
 ser leu his lys asp leu leu gly ala ile ser gly ile ala ser pro tyr thr thr ser

1622 1652  
 ACT CCA AAC ATC AAC AGT GTG AGA AAT GCT GAT TCG AGA GGA TCT CTC ATA AGC ACA GAT  
 thr pro asn ile asn ser val arg asn ala asp ser arg gly ser leu ile ser thr asp  
 ref 5.1 and 5.2

1682 1712  
 TCG GGT AAC AGC CTT CCA GAA AGG AAT AGT GAG AAG AGC AAT TCC CTG GAT AAG CAC CAA  
 ser gly asn ser leu pro glu arg asn ser glu lys ser asn ser leu asp lys his gln

1742 1772  
 CAA AGT AGC ACA TTG GGA AAT TCC GTG GTT CGC TGT GAT AAA CTT GAC CAG TCT GAG ATT  
 gln ser ser thr leu gly asn ser val val arg cys asp lys leu asp gln ser glu ile

1802 1832  
 AAG AGC CTA CTG ATG TGT TTC CTC TAC ATC TTA AAG AGC ATG TCT GAT GAT GCT TTG TTT  
 lys ser leu leu met cys phe leu tyr ile leu lys ser met ser asp asp ala leu phe

1862 1892  
 ACA TAT TGG AAC AAG GCT TCA ACA TCT GAA CTT ATG GAT TTT TTT ACA ATA TCT GAA GTC  
 thr tyr trp asn lys ala ser thr ser glu leu met asp phe phe thr ile ser glu val  
 ref 6.1

1922 1952  
 TGC CTG CAC CAG TTC CAG TAC ATG GGG AAG CGA TAC ATA GCC AGG AAC CAG GAG GGG TTG  
 cys leu his gln phe gln tyr met gly lys arg tyr ile ala arg asn gln glu gly leu

1982 2012  
 GGA CCC ATA GTT CAT GAT CGA AAG TCT CAG ACA TTG CCT GTT TCC CGT AAC AGA ACA GGA  
 gly pro ile val his asp arg lys ser gln thr leu pro val ser arg asn arg thr gly

2042 2072  
 ATG ATG CAT GCC AGA TTG CAG CAG CTG GGC AGC CTG GAT AAC TCT CTC ACT TTT AAC CAC  
 met met his ala arg leu gln gln leu gly ser leu asp asn ser leu thr phe asn his

2102 2132  
 AGC TAT GGC CAC TCG GAC GCA GAT GTT CTG CAC CAG TCA TTA CTT GAA GCC AAC ATT GCT  
 ser tyr gly his ser asp ala asp val leu his gln ser leu leu glu ala asn ile ala

2162 2192  
 ACT GAG GTT TGC CTG ACA GCT CTG GAC ACG CTT TCT CTA TTT ACA TTG GCG TTT AAG AAC  
 thr glu val cys leu thr ala leu asp thr leu ser leu phe thr leu ala phe lys asn  
 ref 7.1

2222 2252  
 CAG CTC CTG GCC GAC CAT GGA CAT AAT CCT CTC ATG AAA AAA GTT TTT GAT GTC TAC CTG  
 gln leu leu ala asp his gly his asn pro leu met lys lys val phe asp val tyr leu

2282 2312

FIG. 6A (cont.)



TGT TTT CTT CAA AAA CAT CAG TCT GAA ACG GCT TTA AAA AAT GTC TTC ACT GCC TTA AGG  
cys phe leu gln lys his gln ser glu thr ala leu lys asn val phe thr ala leu arg

2342

2372

TCC TTA ATT TAT AAG TTT CCC TCA ACA TTC TAT GAA GGG AGA GCG GAC ATG TGT GCG GCT  
ser leu ile tyr lys phe pro ser thr phe tyr glu gly arg ala asp met cys ala ala

2402

2432

CTG TGT TAC GAG ATT CTC AAG TGC TGT AAC TCC AAG CTG AGC TCC ATC AGG ACG GAG GCC  
leu cys tyr glu ile leu lys cys cys asn ser lys leu ser ser ile arg thr glu ala

2462

2492

TCC CAG CTG CTC TAC TTC CTG ATG AGG AAC AAC TTT GAT TAC ACT GGA AAG AAG TCC TTT  
ser gln leu leu tyr phe leu met arg asn asn phe asp tyr thr gly lys lys ser phe

2522

2552

GTC CGG ACA CAT TTG CAA GTC ATC ATA TCT GTC AGC CAG CTG ATA GCA GAC GTT GTT GGC  
val arg thr his leu gln val ile ile ser val ser gln leu ile ala asp val val gly

2582

2612

ATT GGG GAA ACC AGA TTC CAG CAG TCC CTG TCC ATC ATC AAC AAC TGT GCC AAC AGT GAC  
ile gly glu thr arg phe gln gln ser leu ser ile ile asn asn cys ala asn ser asp

2642

2672

CGG CTT ATT AAG CAC ACC AGC TTC TCC TCT GAT GTG AAG GAC TTA ACC AAA AGG ATA CGC  
arg leu ile lys his thr ser phe ser ser asp val lys asp leu thr lys arg ile arg

2702

2732

ACG GTG CTA ATG GCC ACC GCC CAG ATG AAG GAG CAT GAG AAC GAC CCA GAG ATG CTG GTG  
thr val leu met ala thr ala gln met lys glu his glu asn asp pro glu met leu val

2762

2792

GAC CTC CAG TAC AGC CTG GCC AAA TCC TAT GCC AGC ACG CCC GAG CTC AGG AAG ACG TGG  
asp leu gln tyr ser leu ala lys ser tyr ala ser thr pro glu leu arg lys thr trp

2822

2852

lxxxxxxxxxxxxxxxx Predicted

CTC GAC AGC ATG GCC AGG ATC CAT GTC AAA AAT GGC GAT CTC TCA GAG GCA GCA ATG TGC  
leu asp ser met ala arg ile his val lys asn gly asp leu ser glu ala ala met cys

Transmembrane Domain xxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxx

TAT GTC CAC GTA ACA GCC CTA GTG GCA GAA TAT CTC ACA CGG AAA GGC GTG TTT AGA CAA  
tyr val his val thr ala leu val ala glu tyr leu thr arg lys gly val phe arg gln

2942

2972

GGA TGC ACC GCC TTC AGG GTC ATT ACC CCA AAC ATC GAC GAG GAG GCC TCC ATG ATG GAA  
gly cys thr ala phe arg val ile thr pro asn ile asp glu glu ala ser met met glu

ref 8.1

3002

3032

GAC GTG GGG ATG CAG GAT GTC CAT TTC AAC GAG GAT GTG CTG ATG GAG CTC CTT GAG CAG  
asp val gly met gln asp val his phe asn glu asp val leu met glu leu leu glu gln

3062

3092

TGC GCA GAT GGA CTC TGG AAA GCC GAG CGC TAC GAG CTC ATC GCC GAC ATC TAC AAA CTT  
cys ala asp gly leu trp lys ala glu arg tyr glu leu ile ala asp ile tyr lys leu

Fig. 6A (cont.)

ref 9.1

3122 ATC ATC CCC ATT TAT GAG AAG CGG AGG GAT TTC TTT GAA GAT GAA GAT GGA AAG GAG TAT  
 ile ile pro ile tyr glu lys arg arg asp phe phe glu asp glu asp gly lys glu tyr

3182 3212  
 ATT TAC AAG GAA CCC AAA CTC ACA CCG CTG TCG GAA ATT TCT CAG AGA CTC CTT AAA CTG  
 ile tyr lys glu pro lys leu thr pro leu ser glu ile ser gln arg leu leu lys leu  
 ref 10.1

3242 3272  
 TAC TCG GAT AAA TTT GGT TCT GAA AAT GTC AAA ATG ATA CAG GAT TCT GGC AAG GTC AAC  
 tyr ser asp lys phe gly ser glu asn val lys met ile gln asp ser gly lys val asn

3302 3332  
 CCT AAG GAT CTG GAT TCT AAG TAT GCA TAC ATC CAG GTG ACT CAC GTC ATC CCC TTC TTT  
 pr lys asp leu asp ser lys tyr ala tyr ile gln val thr his val ile pro phe phe

3362 3392  
 GAC GAA AAA GAG TTG CAA GAA AGG AAA ACA GAG TTT GAG AGA TCC CAC AAC ATC CGC CGC  
 asp glu lys glu leu gln glu arg lys thr glu phe glu arg ser his asn ile arg arg

3422 3452  
 TTC ATG TTT GAG ATG CCA TTT ACG CAG ACC GGG AAG AGG CAG GGC GGG GTG GAA GAG CAG  
 phe met phe glu met pro phe thr gln thr gly lys arg gln gly gly val glu glu gln  
 ref 11.1

3482 3512  
 TGC AAA CGG CGC ACC ATC CTG ACA GCC ATA CAC TGC TTC CCT TAT GTG AAG AAG CGC ATC  
 cys lys arg arg thr ile leu thr ala ile his cys phe pro tyr val lys lys arg ile

3542 3572 lxxxxxxx Coiled-coil 1 xxxxxx  
 CCT GTC ATG TAC CAG CAC CAC ACT GAC CTG AAC CCC ATC GAG GTG GCC ATT GAC GAG ATG  
 pro val met tyr gln his his thr asp leu asn pro ile glu val ala ile asp glu met

3602 xxxxxxxx Coiled coil 1 cont'd xxxx 3632 xxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxx  
 AGT AAG AAG GTG GCG GAG CTC CGG CAG CTG TGC TCC TCG GCC GAG GTG GAC ATG ATC AAA  
 ser lys lys val ala glu leu arg gln leu cys ser ser ala glu val asp met ile lys  
 ref 12.1

3662 xxxxxxxxxxxxxxxxxxxxxxxx 1 3692  
 CTG CAG CTC AAA CTC CAG GGC AGC GTG AGT GTT CAG GTC AAT GCT GGC CCA CTA GCA TAT  
 leu gln leu lys leu gln gly ser val ser val gln val asn ala gly pro leu ala tyr

3722 3752  
 GCG CGA GCT TTC TTA GAT GAT ACA AAC ACA AAG CGA TAT CCT GAC AAT AAA GTG AAG CTG  
 ala arg ala phe leu asp asp thr asn thr lys arg tyr pro asp asn lys val lys leu

3782 3812 lxxxxxxxxxxxxxxxxxxxxx  
 CTT AAG GAA GTT TTC AGG CAA TTT GTG GAA GCT TGC GGT CAA GCC TTA GCG GTA AAC GAA  
 leu lys glu val phe arg gln phe val glu ala cys gly gln ala leu ala val asn glu

3842 xxxxxxxx Coiled coil 2 xxxxxxxxxx 3872 xxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxx  
 CGT CTG ATT AAA GAA GAC CAG CTC GAG TAT CAG GAA GAA ATG AAA GCC AAC TAC AGG GAA  
 arg leu ile lys glu asp gln leu glu tyr gln glu glu met lys ala asn tyr arg glu

3902 xxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxx 3932 xxxl

FIG. 6A(cont.)

ATG GCG AAG GAG CTT TCT GAA ATC ATG CAT GAG CAG ATC TGC CCC CTG GAG GAG AAG ACG  
met ala lys glu leu ser glu ile met his glu gln ile cys pro leu glu glu lys thr

3962

3992

AGC GTC TTA CCG AAT TCC CTT CAC ATC TTC AAC GCC ATC AGT GGG ACT CCA ACA AGC ACA  
ser val leu pro asn ser leu his ile phe asn ala ile ser gly thr pro thr ser thr

4022

!xxxx PBM xxxxx!

ATG GTT CAC GGG ATG ACC AGC TCG TCT TCG GTC GTG TGA TTA CAT CTC ATG GCC CGT GTG  
met val his gly met thr ser ser ser ser val val STP

4082

4112

TGG GGA CTT GCT TTG TCA TTT GCA AAC TCA GGA TGC TTT CCA AAG CCA ATC ACT GGG GAG

4142

4172

ACC GAG CAC AGG GAG GAC CAA GGG GAA GGG GAG AGA AAG GAA ATA AAG AAC AAC GTT ATT

4202

4232

TCT TAA CAG ACT TTC TAT AGG AGT TGT AAG AAG GTG CAC ATA TTT TTT TAA ATC TCA CTG

4262

4292

GCA ATA TTC AAA GTT TTC ATT GTG TCT TAA CAA AGG TGT GGT AGA CAC TCT TGA GCT GGA

4322

4352

CTT AGA TTT TAT TCT TCC TTG CAG AGT AGT GTT AGA ATA GAT GGC CTA CAG AAA AAA AAG

4382

4412

GTT CTG GGA TCT ACA TGG CAG GGA GGG CTG CAC TGA CAT TGA TGC CTG GGG GAC CTT TTG

ref 13.1

4442

4472

CCT CGA CTC GTG CCG GAA ATC TGA TCG TAA TCA GGG TAC AGA ACT TAC TAG TTT TGT CTA

4502

4532

GGA GTA TGT TGT ATG ACT AGG ATT TGT GCT ATT ATC TCA TTC AAC AAC ATA GAG CAA GAA

4562

4592

TAG TGA GCT AAC TGA GCT AGA CAC TCA ATT AAT CCG CTA CTG GCT TCA AGT CAG AAC TTT

ref 14.1

4622

4652

GTC ATT AAT CAT CGA CTC CGG GAC GGT CAT ATA TGT ATT ACA TTT CTA CAT TTT TAA TAC

4682

4712

TCA CAT GGG CTT ATG CAT TAA GTT TAA TTG TGA TAA ATT TGT GCT GGT CCA GTA TAT GCA

4742

4772

ATA CAC TTT AAT GGT TTA TTC TTG TCA TAA AAA TGT GCA ATA TGG AGA TGT ATA CAA GTC

4802

TTT ACT

Fig. 6A (cont.)

## BAC sequences of Human CLASP 2

### Ref 1.1

Sequence of BAC4 using primer HC2AS2, which spans nucleotides 327-346 of the cDNA. Exon sequence is underlined and represents nucleotides 356-375.

TTTCTACAGNGTNTACTCAGGTATGTGCTCCTTCAACAAAATTAGCAGTTGCTGCTCTG  
TGACAAAGTTTGCACCATTTTGAAGAAGAAAAAATCCTAATGTGTTATATTACTATA  
TTTTTACTCTATAGATCTTTTTCTAAAGAAAGAAAGTACAACCTGAAGTGCTTATATGTA  
TTCATATAAATGACTAGTACAAGCATCATTTTGAACAGATTTCCCCTTTCATTGGAGG  
ATCTTCTTGATGTTATTTGTACACGATCAATTTTGTAGTCTTAATAAGATGAGGCTGGGTG  
TGGTGGCTCACACCTGTAATCCTAGCATTTTGGAGGCCAAGGTGGGCAGATCACTTTAG  
CCCAGGGGTTTGAGACCAGCCTGGCCAACATGGCAAAACCTTGTCTCTACAAAAATAC  
NAAAATTATCCAGGCATGGTGTATGTGTGCCTGTAGTCCCAACTNCCTAGGAGGCTAGG  
GGTAGGGGGATTGCAAGAGGCTGGGAGGGTCAAAGCCCNAANTGAGCCATTGGTNC  
ATGTCACCTTGGACCCCAAGCNGGGGNGANCAAGAGCAAAGGACTNNTGTNNTTTAN  
AAAAAAAACCGGGCTACCATACNNACCAACCCNACCTACCCNACCTTTCCANNTT  
AAAANAAGGCTTTGNCTTGCANAGGAAAAANCAAAATNNCC

### Ref 1.2

Sequence of BAC26 using primer HC2AS2, which spans nucleotides 327-346 of the cDNA. Exon sequence is underlined and represents nucleotides 351-375.

TCTGGTTTCTACAGTGTATACTNAGGTATGTGCTCCTTNAACAAAATTAGCAGTTGCTG  
CTCTGTGACAAAGTTTGCACCATTTTGAAGAAGAAAAAATCCTAATGTGTTATATTA  
CTATATTTTACTCTATAGATCTTTTTCTAAAGAAAGAAAGTACAACCTGAAGTGCTTAT  
ATGTATTATATAAATGACTAGTACAAGCATCATTTTGAACAGATTTCCCCTTTCATT  
GGAGGATCTTCTTGATGTTATTTGTACACGATCAATTTTGTAGTCTTAATAAGATGAGGC  
TGGGTGTGGTGGCTCACACCTGTAATCCTAGCATTTTGGAGGCCAAGGTGGGCAGATC  
ACTTTAGCCCAGGGGTTTGAGACCAGCCTGGCCAACATGGCAAAACCTTGTCTCTACA  
AAAATACAAAATTATCCAGGCATGGTGTATGTGTGCCTGTAGTCCCAGCTACCTAGGA  
GGCTAGGGTAGGGGGATTGCAAGAGGCTNGGAGGTCAAAGGCCCGCAGTGAGCCATGG  
TCATGTCACTGCACCCCCAGCCAGGGCCGACAGGAGCAAGACTNNTGTNTCAAAAAAA  
AACAGNAACCAACANCCAACAACAACNACCTTTCNGCAAAANAAGCTTGCTNCA  
ANGAAACCAAATGNCTTCTTNTTTTCCCCCN

### Ref 1.3

Sequence of BAC26 using primer HC2AS2, which spans nucleotides 327-346 of the cDNA. Exon sequence is not found within this sequence. This sequence most likely represent intron sequence since this sequence matches the intron sequence found in the previous two BAC sequences.

AGNNNNNCCCNTACNCCACTTTTAACCTTTTGAAAACACAGTGTNTNCTCAANTATGC  
GCTCCTTCACATATTAGCAGTTGCTGCTCTGTGACATAGTTGCACCATTNTGCAAGAAG  
AAAAAATCCTAAGTGTNATATCACTATATNNNTACTCTATAGATCTTNTCTAAAGAAAG  
AAAGTCAACTGATGTGCTTATATGTATNCATATAAATGACTAGTACATGCATCATTTTG  
CAACAGATNTCTCCTCACATTGGAGGATCTTCTNGANGNATTCGACACGATNANTATTA  
GTCTNAATAAGATGANGCTGGTGTGGNGGTACACTGNATCTAGCATNTGGANGCATGT

Flt. 6A (cont.)

GGCAGACACTTANCCNCGGTNGAGACAGCTGTCACTGNCNAACTGTCTCTNTAAANCA  
AANNCTCCGCNGGNGATGGGCTGAGCCAGTCTAGNNGCTAGNTAGNGATGNNGAGN  
TGTNGCACGNCGAGNGAGCATGNTCTGTACTGACTCATCAGGCGNCNACACGNTCTGT  
TCNAAAACATACCCACACACACTCNCACCTNCGCAAAATTGCTCTNNAAANATGCTTNT  
TTCACACNGNTNCAATCNCCTATATNNTCTTCTATTCTNACGNTNATTANNATCTTN  
CNCTGCANAAACNATNCGNCCACCTNNANNACCTTANGCTTNGTTTCACGCTTATAGCTC  
CCCTACACNTNNCAGCNNTTNCNNGTGAAGGGCCNCCCGAATCTACGANCACTACTCTC  
TCCGTATATNGCCTCGGTCCANCGCCATCTGCTGTNTNCTCNCCTNCGCNNTTNANCNG  
TNCGCTATCTCTNNNCCGGATCCNCCCATATNNTNNTCTACTTANAGCGTAANNTNT  
NCNCNCACTANTCACAACCTTNTNCTNNAACCTCTATCTNCTCCTCTCTACCACCTCACT  
TACTACCTNTTCACNCANTCTCCTTCNCTNTCCACTGATCTCCACATAGCTGCTNTACTC  
GCCANTTTATCATATNCACACNCTCTACGCTNNNTNT

#### Ref 2.1

Sequence of BAC4 using primer HC2S1, which spans nucleotides 1107-1126 of the cDNA. Exon sequence is underlined and represents nucleotides 1079-1097.

CTTGTATTNAAAGAGGGTCTGCAGGAAGAAGTGTGTAGTCATAAATACCTCACTGGAT  
ATTTTATACAGGATTCTAAAAAACCTATTAGCAATAGTATGCTAGAAATAGTCATTAGC  
TTCTTGACCTTCTTAGAACTGCACACTCTATTGCACTGTACAGATTTCAAGGATGGCTGC  
AGGGATTGATTTGAAAACTAAGGACACATTTCAATAAACAATGTCTTCAATTGATTTTT  
AGGGCTCCTCCTACTTCAATGAAGGACTTCAGGTAGCTTATAATTACAGACACAGGCTC  
AATAACAATAAAAAAATTAGTAAGGCAGAGCTTTAAAAAAGGAAAAAGATAA  
TTCTACCAGAGAAAGGCTACATGGTGACTTCTGTTACCAGTAACAACCCCGCACTACC  
TTTGGGTCTCCAGGAGCAAAACAGCTAATGTAGTTGTTGATCTGCTTGAAGACAAAGC  
ECCTGTCCATGAAGGTGAAACATCTCTGTGGAGGAAAAACAAGCAAAAAAGTTATTTCA  
GGTCCAAACATTTTCGGAATTTGGATTCAAAGCAGGCATTTATTGCTAATAAGTTTATC  
CACTGACATAAAAAACATGCCTTCAACATTGCCAGAGCACCTACTCTATTNTAGTCNCN

#### Ref 3.1

Sequence of BAC4 using primer C96AS, which spans nucleotides 1443-1452 of the cDNA. Exon sequence is underlined and represents nucleotides 1370-1422.

AATCAGCAGACCAAACAGAGGCAGGTAGAGGGTGGCTATCCTTGCCCTGATGGCTCTGA  
AAAGAAGACACACATGGTAAGTTTGACCCAGGATTCTGAGAACCGAACTAAGTTGGTG  
CTGACCATCTCCTTTATTTGGATCCTTCCTATAAAGACAGATATTTGATTTTAGTCCCAA  
AATAGAGCAAAATCTTAGTGCTGTTACCATGAATTTTCTAACTGATTACTTTCTTTACAC  
CACTTAAAATAAAGGACATTATCAATGCACATTCCTTCCATTGGGGACCACTCACCTT  
GAAGCATATCTGTCATCAAAAGAATGCTTTATCAGCAGGTTCTTGAGCACACTGATGGC  
GATCAGACGGACCTCCCGGAACTCCTGGAGGGCTGTCCCCACCTCCCTNAGTAACAGT  
CCCACCAAGAAGTGGTTTCTGCAGAACTCATCTGTTAATGAGTAGTCAAGCTGGGAGG  
TCTGAAATGAGGATAGAACTACTTTGNGTTAGGAAAGATGCAATGCTCTTTTGAATA  
AAACAAACAAACCAAACNAACAAAAAATAAGACCCATCCTTNTGNATTTCAA  
GCCACCTGGGGTNGGTCAAAGAGATGATCAGNANTTTGGCNTTNAAATGAAGAAAG  
AAATNAATTNTCCAGGGGNTGTTCTNCTTTTAGCACANGGAGGGATNTTAANTGAAA  
ACCAATTTAAATCCAATTNAGGNG

#### Ref 4.1

Fig. 6A (cont.)

Sequence of BAC4 using primer C2AS5, which spans nucleotides 1716-1735 of the cDNA. Exon sequence is underlined and represents nucleotides 1602-1703.

TTCCTTTCTGCAAGGCTGTTCCCGAATCTGTGCTTATGAGAGATCCTCTCGAATCAGCA  
TTTCTCACACTGTTGATGTTTGGAGTTGAGGTTGTATATGGAGAAGCTAAATGGAAATC  
AAGCCAACAATAAAGTTTTATTAAGACAGAACAAAATAAAGATGAGTACTGAACTTTA  
AGGGAAATTGCTTTTATTGCACTTATTTTTTCTGTTAGGAAGTTGGCTCAAGAGTTGCAT  
TCCATTACTTCACCTTTAAAGAACCAGGTCATATACAATGAGATAAAAAGAACTAGT  
CTGAAACATTCAGATGTAAACATCAATTCACCTTGTTAGAAACCACCTTTGATCGCTAAA  
GACTAAATGCATACCTGTTTCAGAATGTGATAGAATGAAGACTTAAAAAAATTAAAAG  
ATAAATCCACCTACAACCTATCAAATCACAAAATTAAACCACACAACAACTTGTAGCA  
TTCAAACCTGGTAATAAAACACTGAGGAGCCTACCCAACCTCTGAGGGGTGTGATGGGGTA  
TTTTAAATTTTCGAGGAGAACACAGTGATATGTGACCTCAGCCAGAAGCTGCTGTTTNA  
GCAGCAGGTTGGTGCTATGCTCCTTTTTGAAGACATATTTGTGAAGCTGGGTATTTTG  
GGGCCTGCTTATGATAAAAANGGCAAGGTNTTCAATGNAGGGGN

#### Ref 4.2

Sequence of BAC26 using primer C2AS5, which spans nucleotides 1716-1735 of the cDNA. Exon sequence is underlined and represents nucleotides 1602-1703.

TTCCTTTCTGGAAGGCTGTTACCCGAATCTGTGCTTATGAGAGATCCTCTCGAATCAGC  
ATTTCTCACACTGTTGATGTTTGGAGTTGAGGTTGTATATGGAGAAGCTAAATGGAAAT  
CAAGCCAACAATAAAGTTTTATTAAGACAGAACAAAATAAAGATGAGTACTGAACTTT  
AAGGGAAATTGCTTTTATTGCACTTATTTTTTCTGTTAGGAAGTTGGCTCAAGAGTTGC  
ATTCCATTACTTCACCTTTAAAGAACCAGGTCATATACAATGAGATAAAAAGAACTA  
GTCTGAAACATTCAGATGTAAACATCAATTCACCTTGTTAGAAACCACCTTTGATCGCTA  
AAGACTAAATGCATACCTGTTTCAGAATGTGATAGAATGAAGACTTAAAAAAATTAAA  
AGATAAATCCACCTACAACCTATCAAATCACAAAATTAAACCNCAACAACAACTTGTAG  
CATTCAAACCTGGTAATAAAACACTGAGGAGCCTACCCAACCTTTGAGGGGTGTCAATGG  
GGTNTTTTTAAATTTTTCGNGGGANANCCCAAGTGNTATGGTGACCTTCACCCAAGAAGC  
TTGTTTGTTTACCAAGCNAGGTTGNNCTNTGCTCCTTTTTAGAAANACNNTATTTTNNN  
AAATNCTGGNTTTTTTNNNGGCCCCCTNCNTTNT

#### Ref 5.1

Sequence of BAC4 using primer C2S6, which spans nucleotides 1686-1705 of the cDNA. Exon sequence is underlined and represents nucleotides 1724-1736.

TTCCTGGATAAGGTAATTGCTTTTACCCAACACAAATGTTTCTTATAATCAATGGATTT  
AGCCCAAAGTAAACGTACTTCATGTTCTAGTGCCTTTTAAGTGTGACCTTTTGTTTTTTT  
CTAAACCACCCGGCTGACCTGGAGTAGGTGATGAGAGCTTTAAGGTTGGGGCCCATTC  
CTTGAAGTGCTCTGATTCCTGTTTCCAGTACCTCAGATCCTGGGCAGGGTTTGCAGTGG  
AGCGTCTTGAGTGAATGGCTCTGGTGGGTTGAACGGGGAGGGACTCAAATGCTGCCC  
ATCTCAATTTCTGTAGTCTTTTTATTTATTTATTTATTTTTTGAGACAGAGTCTCGCTCT  
GTCGCCCAGGCTGGAGTACAGCGGCACGATCTCAATTNACTGCAACCTCCGCCTCC:TG  
GGTTCAAACGACTCCTCTGCCTCAGCCTCCCCAGCAGC:TGGGACCACAGGCACAAGCC  
ACCACCGCCCGGCTAATTTTTGTNTTTTTAGTA:GAGAT:GGGGTTTCACCATATTTGGC  
CAGGCTGGGCTCAAACCTCCTGACC:TCGTCATCCGCNCCCTCGGNCTNCCAAAGTGCTT  
GGGATTNCAGGCNGTGAGCCCACTTACACCTNNGGCAATTCCCTGTNAGTCTTTTTTAC  
CAGAGACACCATCATTCAACACAGCTTTTCCACCCACAA

Fig. 6A (cont.)

### Ref 5.2

Sequence of BAC26 using primer C2S6, which spans nucleotides 1686-1705 of the cDNA. Exon sequence is underlined and represents nucleotides 1712-1736.

TGAGAAGAGCAATTTCTCTGGATAAGGTAATTGCTTTTACCCAACACAAATGTTTCTTAT  
AATCAATGGATTTAGCCCAAAGTAAACGTACTTCATGTTCTAGTGCCTTTTAAGTGTGA  
CCTTTTGTTTTTTTCTAAACCACCCGGCTGACCTGGAGTAGGTGATGAGAGCTTTAAGG  
TTGGGGGCCCATTCCTTGAAGTGCTCTGATTCCTGTTTCCAGTACCTCAGATCCTGGGCA  
GGGTTTGCAGTGGAGCGTCTTGAGTGAATGGCTCTGGTGGGTTGAACGGGGAGGGACT  
CAAAATGCTGCCCATCTCAATTTCTGTAGTCTTTTTATTATTTATTTATTTTGTAGAC  
AGAGTCTCGCTCTGTGCGCCAGGCTGGAGTACAGCGGCACGATCTCAATTCAGTGCAA  
CCTCCGNCCTCCCTGGGTTCAAACGACTCCTCTGNCTNAGNCTCCC:AGCAGCCTGGGAA  
CCACAGGCTCANGCCACCACGCCCCGGCTAATTNTTGTAATTTTNAGTAANAAATTGGG  
GGTTCTACCATNTTGGCCCAAGNCTTGGGCCTAAAAACCTTNCTNACCNTCGNCATTC  
NCNCCCCNACCNTGGGCNCTNCTCAAANGNGCTTGGGGATTANCANNGGCNTTAACC  
CCCCNTATCACCGTGGNCCTTAATTT

### Ref 6.1

Sequence of BAC4 using primer C2S7, which spans nucleotides 1918-1937 of the cDNA. Exon sequence is not found within this sequence. Since the primer is directed against exon sequence we presume that sequence derived from C2S7 is intron sequence.

NAGNGNGGGTTTNAGNCGTTTGAAGCCTGNNACGNGGTGNGTGCTNGAACTCTGTGGG  
CTTTCAGGTAAGTGGGGTATCTGGGAGCCTGCTGTTTGCATTGCTAGTGCATCAGACCAG  
GGCTTTTTCTCCCTGTAGCTGCTACTTATACATAGCTCTAACTGAGATGATTCTCCA  
GACAACTGATGCAGAGCAGCAAAAGCTTCTGCCGTTCTCCCCCTTCTAGGAGTGTCTCCT  
TTCTTTGGAAAGAGATCATGAGGGGCTAGATTGTAATGAAGTGAGGCTCAGTGCTTGA  
GCACATCCGGTAAAAGTTCCAATATATTGGTCATAAAGTTTCTCATTCTTTATAGCAGT  
TAATTTCTCTGGCTCATGAGTTTTCTTAGTTTTAATCTGACTTTTAAATTAATGTCTCCA  
GCACCAAGTCATATCCCCAGGGCAAACCTCAAAGGCATGAGAGGCCAGACTCGGGTCCTG  
GTCATAGCAACCCCTGTCTAGGGCCTTGGTCCCTGCCTCCGCTTGTGTGCTGTGGCGCA  
GGTCCTATGGGGCCCTTAGGAAACAGGACCACCCTGTGCGACCCCCCTACAGAGACCAGC  
CAAGTTTGACATTAGATCACCGTAGCAATGTNTGCAAATTCCAGTTTCTTGCTAAAACA  
GGTTAAGCCTTGCAGCCACTTTATCTGTAAGTGGCNGAGGTTTTGACATAAAA

### Ref 7.1

Sequence of BAC4 using primer C2S8, which spans nucleotides 2143-2162 of the cDNA. Exon sequence is underlined and represents nucleotides 2182-2219.

CTCTCGACACGCTGTTTCTATTAACATTGGCGTTTAAGGTTTGTATCAATTTGCTGTTCTG  
NGGTTCTAGTTTTACCTTTCACATTCATTCTGCTTGGTAAGCTCAGTGAGCACAACTTA  
CTATGTTGCATTTTTACTTCAGCAATTATTTTTGTCCCTGTAAGGAAACCATTAATCTTT  
AAATTCCTTTAATGAAATCATTCCACAGTGAATGGCTTGAATGCCCTGAAATAAAATTT  
AACTGGTCAGTGTGTGCTGCGCGCTTGGGTATGGTGGAAACACGGTCTCTGGAGGCAG  
TTAACTCTTGGCTCGAACCTTGAGGATGGTGAATATAGGCACCTAATCAGGCATTTCTG  
CCTTGAATATCTTTAAATATATCCAAATGTTATAGCGTTTAATTAGATTTTTATGTAGAA  
AGGAGCAATAAACACAAGACACATGTTTTCAGTTTTTTATCTGTTACTGCATTAAATGA

Fig. 6A (cont.)

TAAAAACGTTTTGGAGATAGAAAATGAAAGGGGGTTTTTTTTTTGTCTTGTTTTAAAGTT  
TTAGCAAATAATATTCAAGTAGGTGGAGATGGACTCTTCACCACTCTCCTGTTTTTAGG  
AACCCAATACTTTTTTCACTTCTTGCTAAATGATTACTTCCATTTCTAGCATAGAAAAGGA  
GAAAATTGGAATGAGTGTTTATAT

#### Ref 8.1

Sequence of BAC4 using primer C2S9, which spans nucleotides 2992-3011 of the cDNA. Exon sequence is not found within this sequence. Since the primer is directed against exon sequence we presume that sequence derived from C2S9 is intron sequence

CGCTTTNAAATNCCAGCCGCTACTGCGGGGCGNTNAAATTCGAAACGTGTTGTTNTCTGT  
GATGCCTGGCTCTGATTGTGTGGGATTGGTCATCAGTGGCGGTGGCAGNTGGGGTTCA  
TGGAAGCGGCCATGGGGACTGATGGCAGGCCCTTGATTGCCACCGCAGAGCCTGGCA  
GTGTCTTTGGTCTGCATTCTACCGGCGAAGTCTCATTTACCTCACGTGTTATCTCTTG  
GAAAGCATTCTTTAGCGGGCTGTGTCTACCCTTCCATCCTCTCGTCCAAACTCCCCCTC  
CTTCTCTGTTCTGTCTCCTTCCCATCCTCTTCTCCCCAGTTCTTCTTCCTATGTTCCCTCCT  
CAGTGGTTTCTCTTCTCTGTTTGACTTTCCAAGGTCATTTTGACTGTTCTGCTCCCAA  
CTACAAAGATACTAAAATCTCACCTAACCCTCTTCTTCTTTCTTAATGAAAGAATGTT  
TTCAGTCCATCCCAAATTTGTGTGGACTTCACAAACCTTCTCTAAAATGGAGCCTTTTCT  
CTTCTACTCTTGACTAGNTGGTAAACGCTCCATGTTCTTGCCAGAACTCCCTGGTGA  
GTAGCGTCACTCCCACTTTCTGTGCAGAACCAAGCCTCCTAGAAAACCTCCTTTGCANC  
TGAGTGGGTGGGACACGCCCTTNTTTGGG

#### Ref 9.1

Sequence of BAC4 using primer C2AS10, which spans nucleotides 3276-3295 of the cDNA. Exon sequence is underlined and represents nucleotides 3147-3234.

TTTANACCNATNTATCCGNGTCAGTTANAGGAGTCTCTGAGAAATTTCCGACAGCGGT  
GTGAGTTTGGGTTTCTTGTAATATACTCCTTTCCATCTTCATCTTCAAAGAATCCCTGT  
GACATAAAGCACAAATTAGAGCTATCCCTGAACGTAAGCCCAGGGCTTACCACCTAGGA  
AGCGTTCTTTTATTACAAGGGGGGAAAAAAAGGAATGGGTCTAAAAATCCAGCTGAAAT  
GGGCTTTCTGAATGAGAAAGAAAAATGCTAATAACATGAAGTCTAGGTGCAAAGGTAAA  
GGAAAAACACAACATTGCAAACCTTATTCAAGAATGCAGTCATTAAGTGTTGAGTGAAA  
TGAAAGATTTTGGATACAAGACTAAGCTGTCCCAGGGGAAGTCTAATGGGAGTCAAGCC  
TGTTTCACTTTCCCAAGAAGCAGAACTCACTANAAAATGATGAGCAGCCACGACAGG  
CAGGCTCAGAAAGTGGACATGCCTCCCTTCTCCTGATGGCTNCCATGCACACAGGATTTT  
ATGGCATGAACTGAAGCGTTTGGGGGTCTGGAGTAAGTTTAGTAAAAGTTAGGTAAAG  
CTTGTATAAATTGTATTTTGTCTTACCCGATGAGAAAAAAATATTNAAGACCTGGTA  
GCTTCAATATTCAAGAAAAATATTTTTCATNTCACCCG

#### Ref 10.1

Sequence of BAC4 using primer C2S11, which spans nucleotides 3167-3186 of the cDNA. Exon sequence is underlined and represents nucleotides 3231-3296.

NGNANGTGGAGCCNCGANCCAGGGACAATCTNAACTNCTTAAACTGTACTCGGATNA  
ATTTGGTTCTGAAAATGTCAAAATGATACAGGATTCTGGCAAGGTATTGACCATGTTG  
GANAAAGTTTCATAGCAATGTAATGTTGTGATNCGATTACATATNATATATTTTAAATG  
TNTATAGAAAAAACACANGAAAAATATTAAGGATTGTTGGCCCGTGAGTGGCAGGTG  
TATNTTCTNCTGATCCTTTAGNGCTTCCATTACATGCNTGACATTAAAAAAANCTTTA

Fig. 6A (cont.)



TCGCCTAATTTTTGAAACATCTAATTTTACAAAATAATTAACCGTNTGGCCANGNATAT  
TNTCATTTTTAGGNCCAGCTATTTAGAACTCTGACANAAATGAGGGGCTGTGGCTTNC  
CTNCCTNNACTTGNCCTCTTTTCNNGNATGTACCACATGAACTTGNCNCCTCTTTTCNNC  
TNACCGGGTGGCATGTTANAGGACAGGTTGAAACCNCANTNNGGGCNGGANTTNGGTN  
NAATTGGGACACAATGGTACNANGCTCTATNGGAATNGAACTCTCCCNACNNNCNGT  
GNNCCNTGGGGAAAATGNGNCNNATTCAATTTN

#### Ref 11.1

Sequence of BAC4 using primer C2S12, which spans nucleotides 3474-3493 of the cDNA. Exon sequence is not found within this sequence. Since the primer is directed against exon sequence we presume that sequence derived from C2S9 is intron sequence

AGNANNGTTNNGCAGCTGCANNTCTGGACCCANAGGCCGCANGGGCACGAGCCNGGA  
CACGCTCGGCAAAGAGCTGTCCAGAGGGATTGAGAAGCTTCAGGACTGGAAGGGTCTT  
TCGAGCTCAGTTAGCCACCCCCACACCCATTTAGTTTCACATTTATCTAGTGCTTCCTT  
TTGAATACTTGGGATGTTTTCTGTTGATCTGTTGGCACTTCCTTCTTCCACAAGACCAG  
AAGCTCATATCCAATCTAAGGTCACTTACCCTTCTGAGAATCTGATGAAAATGGCGTGC  
CTTATGTGCCTAGATGCTTTTGACACAGTCTAAGGTGACTTATGGACTCCAGGTCCAG  
CAGCCACACCCAGTCCTGGGTCTCCGCACAGGGAGGGACCCGTCTTCACACACCTGTCT  
CAGGTTCTAGCATTGGGCTGCTTCAGCGGTCTCAGGCTGTGAGTAAATGGGATGTGAG  
CTTGGATCGCCCCACGCTGTTGNCCCCCGGGGGGCTTGGCCAGCTGGCCACTTNGAAAT  
GCCTCCTTTTGCCCAGGAAAGCTCACTGCATTTCAATGGGGNTTNTCCACGAAGTTCAN  
CTTTANGGG

#### Ref 12.1

Sequence of BAC4 using primer C2S13, which spans nucleotides 3645-3664 of the cDNA. Exon sequence is underlined and represents nucleotides 3683-3699.

AGNAAGGTNNCTCANTNAANNCAGCGTGAGNGTTCAGGTGAGCCAGGCACAGCAGGC  
CGGAGGGGCAGCAGGGGACGTCCTTGCCCTGGGTGACTTGAGAGTCGTTTCCACTAAC  
AAGGTCTACTTGAGAGCCTCGGTTTACCAAGTGATCCCTGCTCCCTTCCCCCAACGTNT  
GTGACATTTCTCCTGATATCAGAGGGGGAGGAAACCTCATGATCCCTGCCCCCGCCCC  
ATGAGGACTGACTGTGGGGACAAAGAGCCAGATCTCATAGACTACCCTGATTTGTCAG  
TATTTGGGGAATTCTGGGTGCCTGATTAGAAGCATCAAGACTCTTCTAAATNCAAAGA  
AGTGTGGAGAGCAGTAGATTTTCCTATAAACTGGTGTTGCTGGTTTCTATGAAAATTG  
GATCCAAAAAAGTCCTTAAGTTTACCCTCTTAATGGNATCTTTTGATTAATGGAATTC  
ATTATTTTAATATAGCCCAATCAATCCAATTTTTCTTTATTGGTAGCATTTTTATGTTCTC  
TTTAAAAAATCTTGGNCTACCTCCAAAATTCACAGATGTTCTCCTAGGGTTTTCTCTCC  
TTTTGGTTCAAGCATCCCATTCANGTCTTGCACTCCATTCTGGGG

#### Ref 13.1

Sequence of BAC4 using primer C2S14, which spans nucleotides 4289-4308 of the cDNA. Exon sequence is underlined and represents nucleotides 4321-4448.

GACTTANATTTATTCTTCCTTGCGAGAGTAGTGTTAGAATAGATGGCCTACAGAAAAAAA  
AGGTTCTGGGATCTACATGGCAGGGAGGGCTGCACTGACATTGATGCCTGGGGGACCT  
TTTGCTCGAGGCTGAGCTGGAAAATCTTGAAAATATTTTTTTTTCTGTGGCACATTC  
AGGTTGAATACAAGAACTATTTTTGTGACTATGTTTTTGATGACCTAAGGGAAGTACC  
ATTGTAATTTTTGTACCANTGAACCANGAGATTTAAGTGCTTTTATATTCAATTCCTTGC

Fig. 6A (cont.)

ATTTAAGAAAATATGAAAGCTTAAGGAATTATGTGAGCTTAAAACTAGTCAAGCANTT  
TAGAACCAAAGGCCTATNTTNATAACCGCAACTATGCTNAAAAGNACAAAGTAGTACA  
GNATATTGNTATGTACATATCATTGGTAATACACNCCNGGCNTTCTGTACATATATGT  
ATTACATTTCTACNTTTTAAATACTCCCNTGGGCTTATGCCNTTAAGGTTAANTTGNGAT  
AAATTTNGGCTGTTCCNGTNTATNCNATAACNCTTTT

**Ref 14.1**

Sequence of BAC4 using primer C2AS15, which spans nucleotides 4680-4700 of the cDNA. Exon sequence is underlined and represents nucleotides 4660-4683.

ATGAGAATGTAATACATATATGTACAGAATGCCAGGACTGTATTAACAATGATATGTA  
CATAACAATATACTGTACTACTTTGTACTTTTCAGCATAGTTGCGGTTATTAATATAGG  
CCTTTGGTTCTAAACTGCTTGACTAGTTTTAAGCTCACATAATTCCTTAAGCTTTCATAT  
TTTCTTAAATGCAAGGAAATGAATATAAAAAGCACTAAATCTCCTGGTTCCTGGTACAA  
AAATTACAATGGTCAGTTCCTTAGGTCATCAAAAAGTTCACAAAAATAGTTCTTGT  
ATTCAACCTGAATGTGCCACAGGAAAAAAAAAATATTTTCAAGATTTTCCAGCTCAGC  
CTCGAGGCAAAAGGCCCCAGGCATCAATGTCAGNGCAGCCCTCCTGCCATGTAGATC  
CCAGAACCTTTTTTTTCTGTAGGCCATCTATTCTAACACTACTCTGCAGGGAGAATAAA  
ATCTAAAGNCCAGCTCAAGAGTGCTACCACACCTTTGTTAAAGACACAATGAAAACCTT  
GGATATTGGCAGGNGAGATTTAAAAAAAAAATGTGCCCTTTCTTACCACTCCTATAGNA  
AAGTCTGGTTAAGAAATAACCGTTGGTCTTTATTTTCCTTTTNTTTCCCCTTCCCTTGGG  
NCTTCCTGGGGCTCGG

4683  
4682  
4681  
4680  
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4661  
4660

Fig. 6A (cont.)

|      |                                                              |
|------|--------------------------------------------------------------|
| HC2A | -----                                                        |
| KIAA | ASGNLDKNARFSAIYRQDSNKLSNDDMLKLLADFRKPEKMAKLPVILGNLDITIDNVSSD |
| rat  | -----                                                        |
| HC4  | -----                                                        |
| HC1  | -----                                                        |
| HC3  | -----                                                        |
| HC5  | -----                                                        |

|      |                                                             |
|------|-------------------------------------------------------------|
| HC2A | -----                                                       |
| KIAA | FPNYVNSSYIPTKQFETCSKTPITFEVEEFVPCIPKHTQPYTIYTNHLYVYPKYLYDSQ |
| rat  | -----                                                       |
| HC4  | -----                                                       |
| HC1  | -----                                                       |
| HC3  | -----                                                       |
| HC5  | -----                                                       |

|      |                                                             |
|------|-------------------------------------------------------------|
| HC2A | -----VLHHHQNPEFYDEIK                                        |
| KIAA | KSFAKARNIAICIEFKDSDEEDSQPLKCIYGRPGGPVTRSAFAAVLHHHQNPEFYDEIK |
| rat  | -----                                                       |
| HC4  | -----                                                       |
| HC1  | -----                                                       |
| HC3  | -----                                                       |
| HC5  | -----                                                       |

|      |                                                            |
|------|------------------------------------------------------------|
| HC2A | IELPTQLHEKHHLTFFHVSCDNSSKGSTKKRDVVETQVGYSWLPLLKDGRVVTSEQHI |
| KIAA | IELPTQLHEKHHLTFFHVSCDNSSKGSTKKRDVVETQVGYSWLPLLKDGRVVTSEQHI |
| rat  | -----                                                      |
| HC4  | -----                                                      |
| HC1  | -----                                                      |
| HC3  | -----                                                      |
| HC5  | -----                                                      |

|      |                                                              |
|------|--------------------------------------------------------------|
| HC2A | PVSANLPSGYLGYQELGMGRHYGPEIKWVDGGKPLLKISTHLVSTVYTQDQHLHNFFQYC |
| KIAA | PVSANLPSGYLGYQELGMGRHYGPEIKWVDGGKPLLKISTHLVSTVYTQDQHLHNFFQYC |
| rat  | -----                                                        |
| HC4  | -----                                                        |
| HC1  | -----                                                        |
| HC3  | -----GPGPARSTVSIISLISNSARV                                   |
| HC5  | -----                                                        |

|      |                                                             |
|------|-------------------------------------------------------------|
| HC2A | QKTESGAQALGNELVKYLSLHAMEGHVMIAFLPTILNQLFRVLT-RATQEEVAVNVTRV |
| KIAA | QKTESGAQALGNELVKYLSLHAMEGHVMIAFLPTILNQLFRVLT-RATQEEVAVNVTRV |
| rat  | -----                                                       |
| HC4  | -----MEIQVLIRFLSVILMQLFWVLPNMIHEDDVPISCPMV                  |
| HC1  | -----MSFLPIILNQLFKVLV-QNEEDEITTTVTRV                        |
| HC3  | NRSRSLSNSNPDISGTPTSPDDEVRSIIGSKGLDRSNSWNTGGPKAAPWGSNPPSPAES |
| HC5  | -----                                                       |

Fig. 6B (cont.)

HC2A I IHVVAQCHESHLRSYVKYAYKAEPYVASEYKTVHEELMTTILKPSADFLTSN  
 KIAA I IHVVAQCHESHLRSYVKYAYKAEPYVASEYKTVHEELMTTILKPSADFLTSN  
 rat -----  
 HC4 LFHIVSKCHEEGLDSYLSSFIKYSFRPGKPSAPOAPLIHETLATMMIALLKQSADFLAIN  
 HC1 LPDIVAKCHEEQLDHSVQSYIKFVFKTR---ACKERPVEDLAKNVTGLLK-SNDSPTVK  
 HC3 TQAMDRSCNRMSSHTETSSFLQTLTGRLP----TKKLFHEELALQWVVCSG--SVR---E  
 HC5 -----

Cadherin  
 Cleavage

HC2A KLLRYSWFFFDVLIKSMQAHLIENSKVKLIIRNORFPASYHHAAETVVNMLMPHITQKFGD  
 KIAA KLLKYSWFFFDVLIKSMQAHLIENSKVKLIIRNORFPASYHHAETVVNMLMPHITQKFRD  
 rat -----  
 HC4 KLLKYSWFFFEIIAKSMATYLLLENKIKLTHGQRFPKAYHHALHSLFLAIT-IVESQYAE  
 HC1 HVLKHSWFFFAIILKSMQHLIDTNKIQLERPORFPESYQNELDNLMVLSDHVIWKYKD  
 HC3 SALQQAFFFFELMVKSMVHHLYFNDKLEAFKRSRFPERFMDDIAALVSTIASDIVSRFQK  
 HC5 -----

6.1  
 1.1/1.2/2.1/2.2

HC2A NPEASKNANHSLAVFIKRCFTFMDRGFVFKQIN---NYIS--CFAPGDEKTLFEYKFEFL  
 KIAA NPEASKNANHSLAVFIKRCFTFMDRGFVFKQIN---NYIS--CFAPGDPKTLFEYKFEFL  
 rat -----  
 HC4 IPKESRNVNYSLASFLKCCLTLMDRGFVFNLIN---DYIS--GFSPKDPKVLAEYKFEFL  
 HC1 ALEETRRATHSVARFLKRCFTFMDRGCVFKMVN---NYIS--MFSSGDLKTLQYKFDL  
 HC3 DTEMVERLNTSLAFFLNDLLSVMDRGFVFSLIKSCYQVSSKLYSLPNPSVIVSLRLDFL  
 HC5 -----

2.1

7.1  
 3.1 / 3.2

HC2A RVVCNHEHYIPLNLPM-----PFGKGRIQR-----YQDLQL----DYSLTDEF  
 KIAA RVVCNHEHYIPLNLPM-----PFGKGRIQR-----YQDLQL----DYSLTDEF  
 rat -----  
 HC4 QTICNHEHYIPLNLPM-----AFAPKPLQR-----VQDSNL----EYSLSDEY  
 HC1 QEVCQHEHFIPCLPIRSANIPDPLTPSES-----TQELHASDMPEYSVTNEF  
 HC3 RIICSHEHYVTNLPCSLTTPASPSPSVSSATSSQSGFSTNVQDQKIANMFELS--VPF  
 HC5 -----MNADTAPTSPCPSIS---SQNSSSCSSFQDQKIASMFDRTSRVA

4.1 / 4.2

HC2A CRNHFLVGLLLREVGTALQEFRE----VRLIAISVLKNLLIKHSFDDRYASRSHQARIAT  
 KIAA CRNHFLVGLLLREVGTALQEFRE----VRLIAISVLKNLLIKHSFDDRYASRSHQARIAT  
 rat -----  
 HC4 CKHHFLVGLLLRETSIALQDNYE----IRYTAISVIKNLLIKHAFDTRYQHKNQQAQIAQ  
 HC1 CRKHFLIGILLREVGFALQEDQD----VRHLALAVLKNLMAKHSFDDRYREPRKQAQIAS  
 HC3 RQQHYLAGLVLTELAVILDPDAEGLFGLHKKVINMVHNLSSHDSDPYSDPQIKARVAM  
 HC5 SSTS-SPGLLFTELAAALDAEGEGISEVQRKAVSAIHSLLSSHDLDPKVCVKEVKVIAA

3.1

8.1

HC2A LYLPLFGLLIENVQRINVRDVSPEPVNAG-MTVKDESLALPAVNPLVTPQKGSTLDNSLH  
 KIAA LYLPLFGLLIENVQRINVRDVSPEPVNAG-MTVKDESLALPAVNPLVTPQKGSTLDNSLH  
 rat -----  
 HC4 LYLPLFVGLLIENIQRLAGRDLYSCAAMPNSASRDEFPCG-----FTSP--AN--RGSLS  
 HC1 LYMPLYGMLLDNMPRIYKLDLYPFTVNTSNQGSRDDLTNGGFQSQTAIKHANSVDTSFS  
 HC3 LYLPLIGIIMETVPQLYDFTETHNQGRPICIAATDDYESE-----SG---SMIS  
 HC5 LYLPLVGIIILDALPQLCDFTVADTRRYR---TSGSDEEQE-----GA---GAIT

9.1

4.1 / 4.2

HC2A KDLLGAISGIASPYTTSTPNINSVRNADSRGSLISTDSGNLPERNSEKSNLSDKHQOSS  
 KIAA KDLLGAISGIASPYTTSTPNINSVRNADSRGSLISTDSGNLPERNSEKSNLSDKHQOSS  
 rat -----  
 HC4 TDKDTAYGSFONG-----HGKREDRSGSLIP-EGATGFPPDQGNLTGEN-----TRQS  
 HC1 KDVLNSIAAFSS-----IAISTVNHADSRASLASLDSNPSTNEKSSEKTDNCEKIPRPL  
 HC3 QTVAMAIAGTSVPQ-----LTRPGSFLLTSTSGRQHT-----  
 HC5 QNVALAIAGNNFN-----LKTSG-IVLSSLPYKQYN-----

5.1 / 5.2

10.1

3.1

2.1

|      |                                                               |                         |
|------|---------------------------------------------------------------|-------------------------|
| HC2A | TLGNSVVRCDKLDQSEIKSLLMCFLYILKSMSDDALFTYWN-KASTSELMDFFTISEVCL  |                         |
| KIAA | TLGNSVVRCDKLDQSEIKSLLMCFLYILKSMSDDALFTYWN-KASTSELMDFFTISEVCL  |                         |
| rat  | -----                                                         |                         |
| HC4  | STRSSVSQYNRLDQYEIRSLIMCYLYIVKMISEDTLITYWN-KVSPQELINILILLEVCL  |                         |
| HC1  | ALIGSTLRFDRLDQAETRSLLMCFLHIMKTISYETLIAYWQ-RAPSPEVSDFFSIIIPVCL | 11.1 / 11.2             |
| HC3  | -----TFSAESSRSLICLLWLKN-ADETVLQKWFTDLSVLQLNRLDLLLYLCV         |                         |
| HC5  | -----MLNADTTNLMICFLWIMKN-ADQSLIRKWIADLPSTQLNRILDLLFICV        |                         |
| HC2A | HQFOYMGKRYIARNQEGLG--PIVHDRKS-----QTLPVSRNRTGMM               | 6.1                     |
| KIAA | HQFOYMGKRYIAR-----TGMM                                        |                         |
| rat  | -----                                                         |                         |
| HC4  | FHFRYMGKRNIARVHDAWLSKHFGIDRKS-----QTMPALNRNSGVM               |                         |
| HC1  | QNFRLGKRNIIRKIAAAF--KFVQSTQNNGTLKGSNPSCQTSGLLAQWMHSTSRHEGHK   |                         |
| HC3  | SCFEYKGKKVFERMNSLTFK--KSKDMRAK-----LEEAILGSIGARQEMV           |                         |
| HC5  | LCFEYKGKQSSDKVSTQVLQ--KSRDVKAR-----LEEALLRGEARGEMM            |                         |
| HC2A | HARLQQL-----GSLDNS-----LTFNHSYGHSDADVLHQSLLEANIATEVC          |                         |
| KIAA | HARLQQL-----GSLDNS-----LTFNHSYGHSDADVLHQSLLEANIATEVC          |                         |
| rat  | -----                                                         |                         |
| HC4  | QARLQHL-----SSLESS-----FTLNHSSTTTEADIFHQALLEGNTATEVS          |                         |
| HC1  | QHRSTLPIIRGK--NALSNPKL----LQMLDNTMTSNEIDIVHHVDTEANIATEGC      | 12.1 / 12.2             |
| HC3  | RRSRGQLERSPSGSAFGSQENLRWRKDMTHWRQNTKLDKSRAEIEHEALIDGNLATEAN   | 6.1 / 6.2               |
| HC5  | RRRAPGNDRFP----GLNENLRWKKEQTHWRQANEKLDKTKAELDQREALISGNLATEAH  |                         |
| HC2A | LTALDTLSLFTLAFKNQLLADHGHNPLMKKVFDVYLCFLQKHQSETALKNVFTALRSLIY  | 7.1                     |
| KIAA | LTALDTLSLFTLAFKNQLLADHGHNPLMKKVFDVYLCFLQKHQSETALKNVFTALRSLIY  |                         |
| rat  | -----KLSRGHSPMLKKVFDVYLCFLQKHQSEMALKNVFTALRSLIY               |                         |
| HC4  | LTVLDTISFFTQCFTKTHFLNNDGHNPLMKKVFDIHLAFLKNGQSEVSLKHVFASLRAFIS |                         |
| HC1  | LTILDVLSLFTQTHORQLQOCDCQNSLMKRGFDTYMLFFQVNSATALKHVFASLRLFVC   | 13.1                    |
| HC3  | LIILDTLEIVVQTVS--VTES--KESILGGVLKVLHSMACNQSAVYLQHCFAQALVS     |                         |
| HC5  | LIILDMQENIIQASS--ALDC--KDSLGGVLRVLVNSLNCQSTTYLTHCFATLRLAIA    | 3.1                     |
| HC2A | KFPSTFYEGRADMCAALCYEILKCCNSKLSSIRTEASQLLYFLMRNNFDYTGKKSFVRTH  |                         |
| KIAA | KFPSTFYEGRADMCAALCYEILKCCNSKLSSIRTEASQLLYFLMRNNFDYTGKKSFVRTH  |                         |
| rat  | KFPSTFYEGRADMCASLCYEVLKCCNSKLSSIRTEASQLLYFLMRNNFDYTGKKSFVRTH  |                         |
| HC4  | KFPSAFFKGRVNMCAAFCEVLKCCCTSKISSTRNEASALLYLLMRNNFEYTKRKTFLRTH  |                         |
| HC1  | KFPSAFFQGPADLCGSFCYEVLKCCNHRSRSTQTEASALLYLFMRKNFEFNKQKSIVRSH  |                         |
| HC3  | KFPPELLFEEETEQCADLCLRLLRHCSSSIGTIRSHPSASLYLLMRQNFEIGN--NFARVK | 7.1 / 7.2               |
| HC5  | KFGDLLFEEVEEQCFDLCHQVLHHCSSSMVTRSQCATLYLLMRFSFGATS--NFARVK    |                         |
| HC2A | LQVVISVSQLIADVVGIGETRFOQSLSIINNCANSRDLIKHTSFSSDVKDLTRIRTVLM   |                         |
| KIAA | LQVVISVSQLIADVVGIGETRFOQSLSIINNCANSRDLIKHTSFSSDVKDLTRIRTVLM   |                         |
| rat  | LQVVISVSQLIADVVGIGETRFOQSLSIINNCANSRDLIKHTSFSSDVKDLTRIRTVLM   |                         |
| HC4  | LQIIIAVSQLIADVALSGGSRFQESLFIINNFANSRPMPLARAFPAEVKDLTRIRTVLM   |                         |
| HC1  | LQIIKAVSQLIAD-AGIGGSRFQHSIAITNNFANGDKQMKNSNFPAEVKDLTKRIRTVLM  | 14.1 / 14.2 / 15.1 / 15 |
| HC3  | MQVPMSLSSLVGTSQNFNEEFLRRSLKTILTYAEEDLELRETTFPDQVQDLVFNLMILS   |                         |
| HC5  | MQVTMSLASLVGRAPDFNEEHLRRSLRTILAYSEEDTAMQMTFFPTQVEELCNLSILY    |                         |

|      |                                                      |             |             |
|------|------------------------------------------------------|-------------|-------------|
| HC2A | ATAQMKEHENDPEMLVDLQYSLAKSYASTPELRKTWLD SMARIHVKNGL   | SEAAMCYVHV  |             |
| KIAA | ATAQMKEHENDPEMLVDLQYSLAKSYASTPELRKTWLD SMARIHVKNGL   | SEAAMCYVHV  |             |
| rat  | ATAQMKEHENDPEMLVDLQYSLAKSYASTPELRKTWLD SMARIHVKNGL   | SEAAMCYVHV  |             |
| HC4  | ATAQMKEHEKDPEMLIDLQYSLAKSYASTPELRKTWLD SMAIHVKNGL    | SEAAMCYVHV  |             |
| HC1  | ATAQMKEHEKDPEMLVDLQYSLANSYASTPELRRTWLESMAKIHARNGD    | SEAAMCYIHI  | 16.1 / 16.2 |
| HC3  | DTVKMKEHQEDPEMLIDL MYRIAKGYQTSPDLRLTLWLQN MAGKHSERSN | HAEAAQCLVHS |             |
| HC5  | DTVKMREFQEDPEMLMDL MYRIAKSYQASPDRLTLWLQN MAEKHTKKKC  | YTEAMCLVHA  |             |

|      |          |                                                     |                                         |
|------|----------|-----------------------------------------------------|-----------------------------------------|
|      |          | SH3                                                 |                                         |
| HC2A | TALVAEYI | TRKGV                                               | FRQGCTAFRVITPN                          |
| KIAA | TALVAEYI | TRKEA                                               | VQWEPPLLPHSHSACLRRSRGGVFRQGCTAFRVITPN   |
| rat  | TALVAEYI | TRKEAD                                              | LALQREPPVFPYSHTSCQRKSRGGMFRQGCTAFRVITPN |
| HC4  | AALVAEFI | HRKKL                                               | FPNGCSAFKKITPN                          |
| HC1  | AALIAEYI | KRKGWYKVEKICTASLLSEDPHPCDSNSLLTTPSGGSMFSGMGPFLSITPN |                                         |
| HC3  | AALVAEYI | SMLED                                               | RKYLPGCVTFQNISSN                        |
| HC5  | AALVAEYI | SMLED                                               | HSYLPVGSVSFQNISSN                       |

9.1 / 8.2

|      |                                                               |                                         |             |
|------|---------------------------------------------------------------|-----------------------------------------|-------------|
| HC2A | IDEEASMMEDVGMQD                                               | VHFNEDVLMELLEQCADGLWKAERYELIADIYKLIPI   | 9.1         |
| KIAA | IDEEASMMEDVGMQD                                               | VHFNEDVLMELLEQCADGLWKAERYELIADIYKLIPI   |             |
| rat  | IDEEASMMEDVGMQD                                               | VHFNEDVLMELLEQCADGLWKAERYELIADIYKLIPI   |             |
| HC4  | IDEEGAMKEDAGMMD                                               | VHYSEEVLLLELLEQCVNGLWKAERYEIISEISKLIGPI |             |
| HC1  | IKEEGAAKEDSGMHD                                               | TPYNEINILVEQLYMCGEFLWKSEYELIADVNKPIIAV  | 17.1 / 17.2 |
| HC3  | VLEESAVSDDVVPDEEGICSGKYFTESGLVGLLEQAAASFSMAGMYEAVNEVYKVLPI    |                                         |             |
| HC5  | VLEESVVSSEDTLSPDEGDGVCAGQYFTESGLVGLLEQAAELFSTGGLYETVNEVYKVLPI |                                         |             |

|      |                                       |                                      |                   |       |                |     |
|------|---------------------------------------|--------------------------------------|-------------------|-------|----------------|-----|
|      |                                       | ITAM                                 | ITAM              | ITAM  | ITAM           |     |
| HC2A | YEKRRD                                |                                      |                   |       |                | 9.1 |
| KIAA | YEKRRD                                | FERLAHLYDTLHRAYSKVTEVMHSGRRLGTYFRVAF | FGQAAQYQFTDSETDVE |       |                |     |
| rat  | SMKSGGTLETTHLYDTLHREYSKVTEVITR        |                                      |                   | A     | AGSWDLLPGGLFGQ |     |
| HC4  | YENRREFENLTQVYRTLHGAYTKILEVMHTKKRLLG  |                                      |                   |       | TFRVAFYGO      |     |
| HC1  | FEKQRDFKKLSDLVYDIHRSYLVKVAEVVNSEKRLFG |                                      |                   |       | RYRVAFYGO      |     |
| HC3  | HEANRDAKKLSTIHGKLQEFFSKI              | HQSTG                                | WERMFG            |       | TYFRVGFYG      | 9.1 |
| HC5  | LEAHREFRKLTLTHSKLQRAFD                | SI                                   | VNKDH             | KRMFG | TYFRVGFYG      |     |

|      |                                                                |             |
|------|----------------------------------------------------------------|-------------|
| HC2A | -FFEDEDGKEYIYKEPKLTPLSEISQRLCLKLYSDKFGSENVKMIQDSGKVNPKDLDSKYA  | 10.1        |
| KIAA | GFFEDEDGKEYIYKEPKLTPLSEISQRLCLKLYSDKFGSENVKMIQDSGKVNPKDLDSKYA  |             |
| rat  | GFFEDEDGKEYIYKEPKLTPLSEISQRLCLKLYSDKFGSENVKMIQDSGKVNPKDLDSKFA  |             |
| HC4  | SFFEEEDGKEYIYKEPKLTGLSEISRLRVKLYGEKFGTENVKIIQSDSKVNAKELDPKYA   |             |
| HC1  | GFFEDEEGKEYIYKEPKLTGLSEISQRLCLKLYADKFGADNVKIIQDSNVKVNPKDLDPKYA |             |
| HC3  | TKFGDLDEQEFVYKEPAITKLAEISHRLGFGYGERFGEDVVEVIKDSNPVDKCKLDPNKA   | 10.1 / 10.2 |
| HC5  | SKFGDLDEQEFVYKEPAITKLPEISHRLAEFGQCFGAEFVEVIKDSTPVDKCKLDPNKA    | 4.1         |

|      |                                                              |             |
|------|--------------------------------------------------------------|-------------|
| HC2A | YIQVTHVIPFFDEKELQERKTEFERSHNIRRFMFEMPFTQTGKRQGGVEEQCKRRTILTA | 11.1 / 11.2 |
| KIAA | YIQVTHVIPFFDEKELQERKTEFERSHNIRRFMFEMPFTQTGKRQGGVEEQCKRRTILTA |             |
| rat  | YIQVTHVIPFFDEKELQERKTEFERCHNIRRFMFEMPFTQTGKRQGGVEEQCKRRTILTA |             |
| HC4  | HIQVTVKPYFDDKELTERKTEFERNHNISRNVFEAPYTLGKKQGCIEEQCKRRTILT    |             |
| HC1  | YIQVTVVTPFFEEKEIEDRKTDFEMHHNINRFVFETPFTLSGKKHGGVAEQCKRRTILT  | 18.1        |
| HC3  | YIQITYVEPYFDTYEMKDRITYFDKNYNLRFRMYCTPFTLDGRAHGEHQFQRKTILT    |             |
| HC5  | YIQITYVEPYFDEYEMKDRVITYFEKNFNLRFRMYTTPFTLEGRPRGELHEQYRRNTVLT |             |

FIG. 6B (cont.)

## Coiled-Coil

|      |      |           |          |           |                                       |
|------|------|-----------|----------|-----------|---------------------------------------|
| HC2A | IHC  | FPYVKKR   | IPV      | MYQHHTDLN | IEVAIDEMSKKVAELRQLCSSAEVDMIKLQLKLGSSV |
| KIAA | IHC  | FPYVKKR   | IPV      | MYQHHTDLN | IEVAIDEMSKKVAELRQLCSSAEVDMIKLQLKLGSSV |
| rat  | IHC  | FPYVKKR   | IPV      | MYQHHTDLN | IEVAIDEMSKKVAELRQLCSSAEVDMIKLQLKLGSSV |
| HC4  | SNS  | FPYVKKR   | IPIN     | CEQQINLKE | IDGATDEIKDKTAELOKLCSSSTDVDMIQLQLKLGWV |
| HC1  | SHL  | FPYVKKR   | IQVIS    | QSSTELNE  | IEVAIDEMSRKVSELNQLCTMEEVDMISLQLKLGSSV |
| HC3  | SHAF | PIKTRVNV  | THKE     | IIILTE    | IEVAIEDMQKKTQELAFATHQDPADPKMLQMVLOGSV |
| HC5  | MHAF | PIKTRISVI | QKEEFVLT | IEVAIEDM  | KKKTLQLAVAINQEPDAKMLQMVLOGSV          |

11.1

## Coiled-Coil 2

|      |     |                                                            |
|------|-----|------------------------------------------------------------|
| HC2A | SVQ | VNAGPLAYARAFLDDTNTKRYPDNKVKLLKEVFRQFVEACGQALAVNERLIKEDQLE  |
| KIAA | SVQ | VNAGPLAYARAFLDDTNTKRYPDNKVKLLKEVFRQFVEACGQALAVNERLIKEDQLE  |
| rat  | SVQ | VNAGPLAYARAFLDDTNTKRYPDNKVKLLKEVFRQFVEACGQALAVNERLIKEDQLE  |
| HC4  | SVQ | VNAGPLAYARAFLNDSQASKYPPKKVSELKDMFRKFIQACSI ALELNERLIKEDQVE |
| HC1  | SVK | VNAGPMAYARAFLEETNAKKYPDNQVKLLKEIFRQFADACGQALDVNERLIKEDQLE  |
| HC3  | GTT | VNQGPLEVAQVFLSEIPSDPKLFRHHNKLRLCFKDFTKRCEDALRKNKSLIGPVQKE  |
| HC5  | GAT | VNQGPLEVAQVFLAEIPADPKLYRHHNKLRLCFKEFIMRCGEAVEKNKRLITADQRE  |

11.1 / 12.1

## Coiled-Coil 2

|      |      |                                                           |
|------|------|-----------------------------------------------------------|
| HC2A | YQE  | EMKANYREMAKELSEIMHEQICPLEEKTS-VLPNSLHIFNAISGTPTSTMVHGMTSS |
| KIAA | YQE  | EMKANYREMAKELSEIMHEQLG-----                               |
| rat  | YQE  | EMKANYREIRKELSDIIVPRICPGEDKRATKFPAPHLQRHQRTDNKHSGRVDQFILS |
| HC4  | YHE  | GLKSNFRDMVKELSDIIEHQILQEDTMHSPWMSNTLHVFCASGTSSDRGYGSPRYA  |
| HC1  | YQE  | ELRSHYKDMLSELSTVMNEQITGRDDLK---RGVDQCTRVISKATPALPTVSISS   |
| HC3  | YQRE | LG---KLSS---PZ---                                         |
| HC5  | YQ   | ELKKNYNKLKENLRPMIERKIPELYKPIFRVESQKRDSFHRSSFRCETQLSQGSZ-  |

19.1

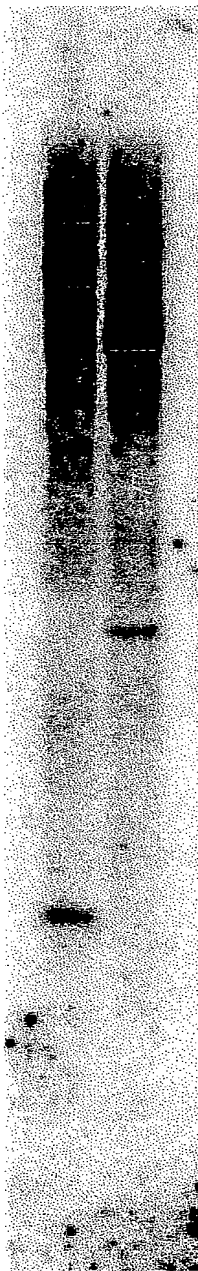
## PBM

|      |       |                                                           |
|------|-------|-----------------------------------------------------------|
| HC2A | SSVV  | -----                                                     |
| KIAA | ----- | -----                                                     |
| rat  | CVTL  | PHEPHVGTFCVMCKLRTTFRANHWFCQAQEEAMNGGREKEPWTVI FNSRFYRSWGK |
| HC4  | EV    | -----                                                     |
| HC1  | SAEV  | -----                                                     |
| HC3  | ----- | -----                                                     |
| HC5  | ----- | -----                                                     |

|      |       |
|------|-------|
| HC2A | ----- |
| KIAA | ----- |
| rat  | VHIF  |
| HC4  | ----- |
| HC1  | ----- |
| HC3  | ----- |
| HC5  | ----- |

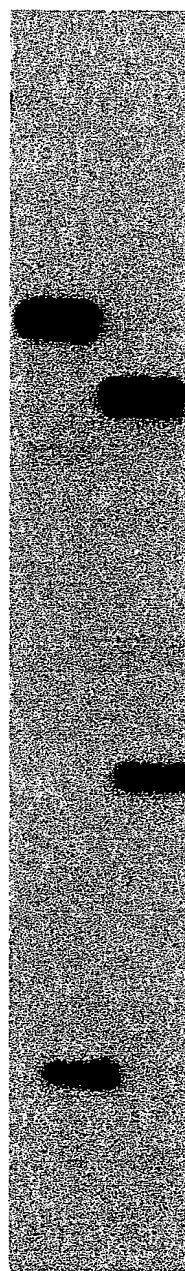
00E70T" 2EB28960

HinDIII  
Eco RI



genomic DNA

Pst I  
Eco RI



BAC 6 DNA

Fig. 7



006707" 48828960

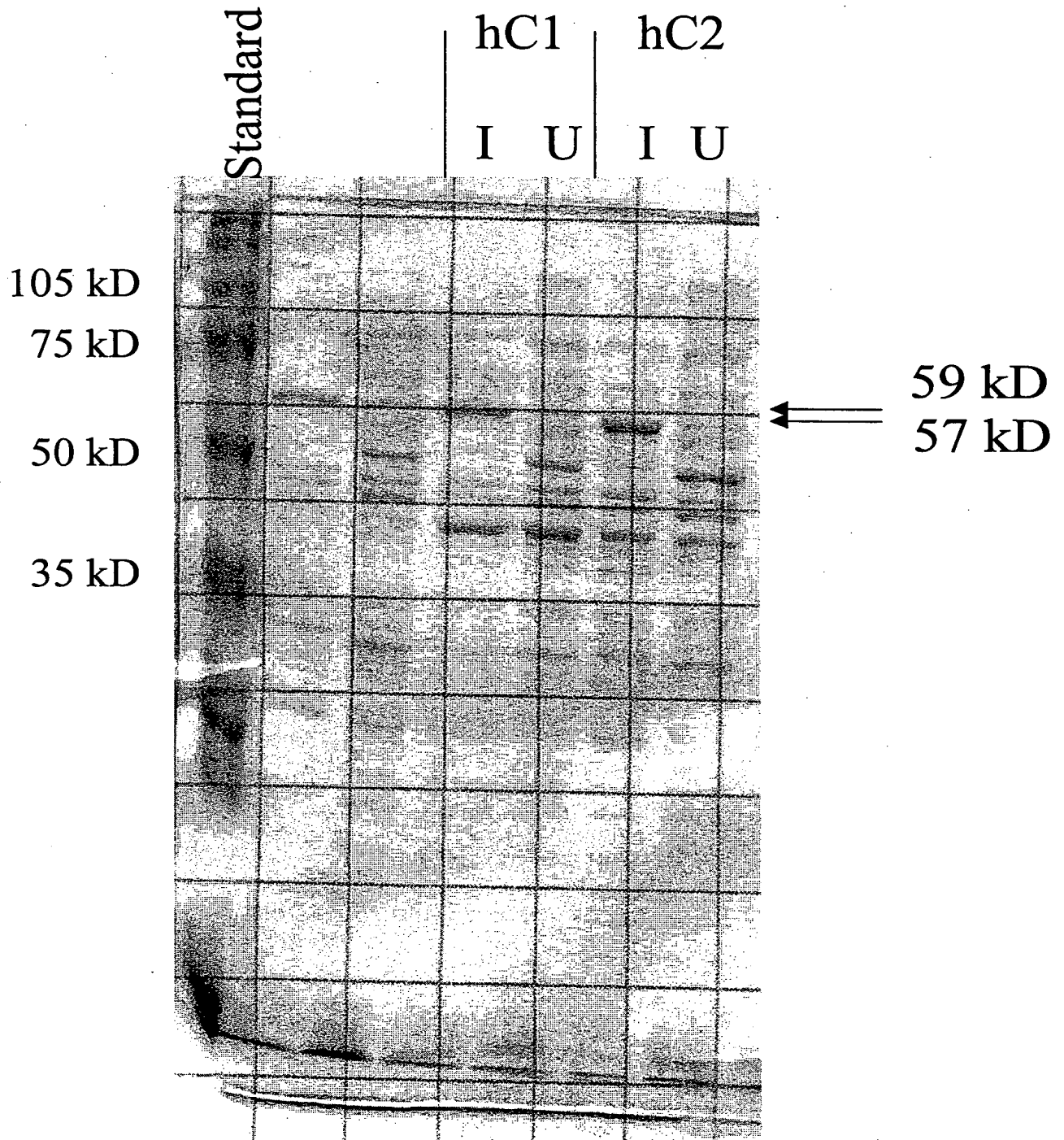


FIG. 8

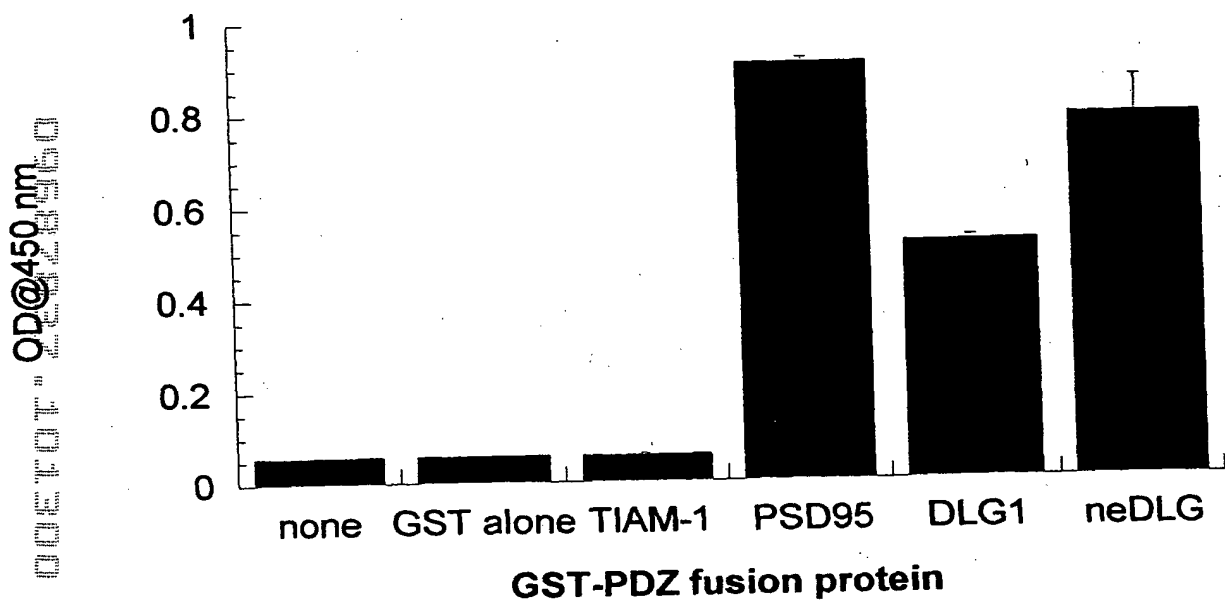


FIG. 9A

fraction maximal binding

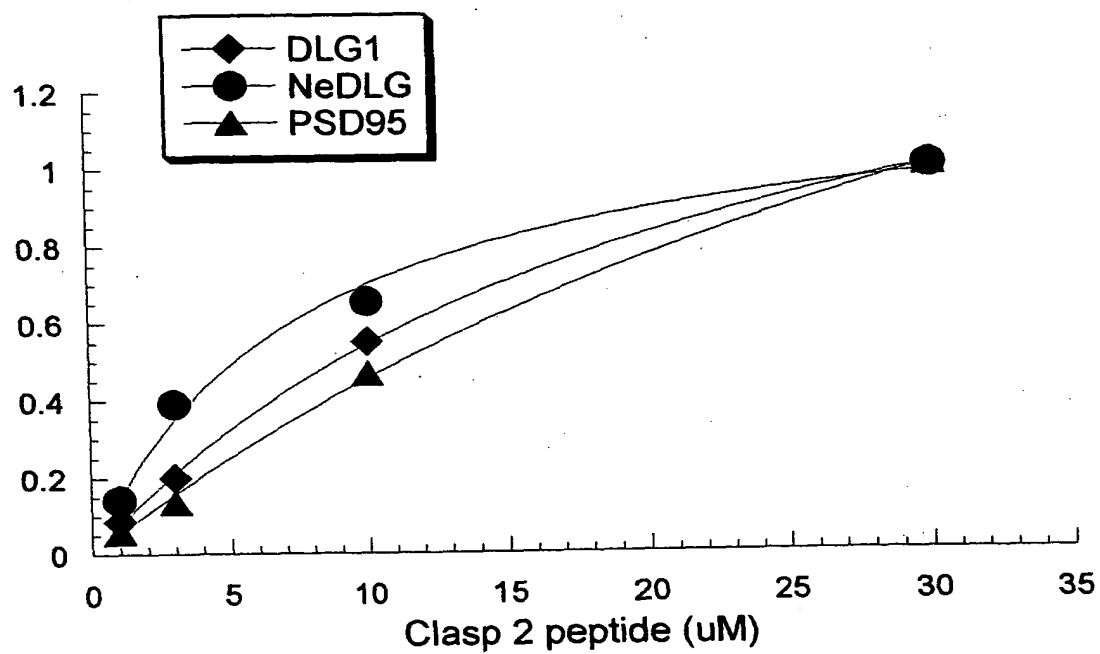


FIG. 9B

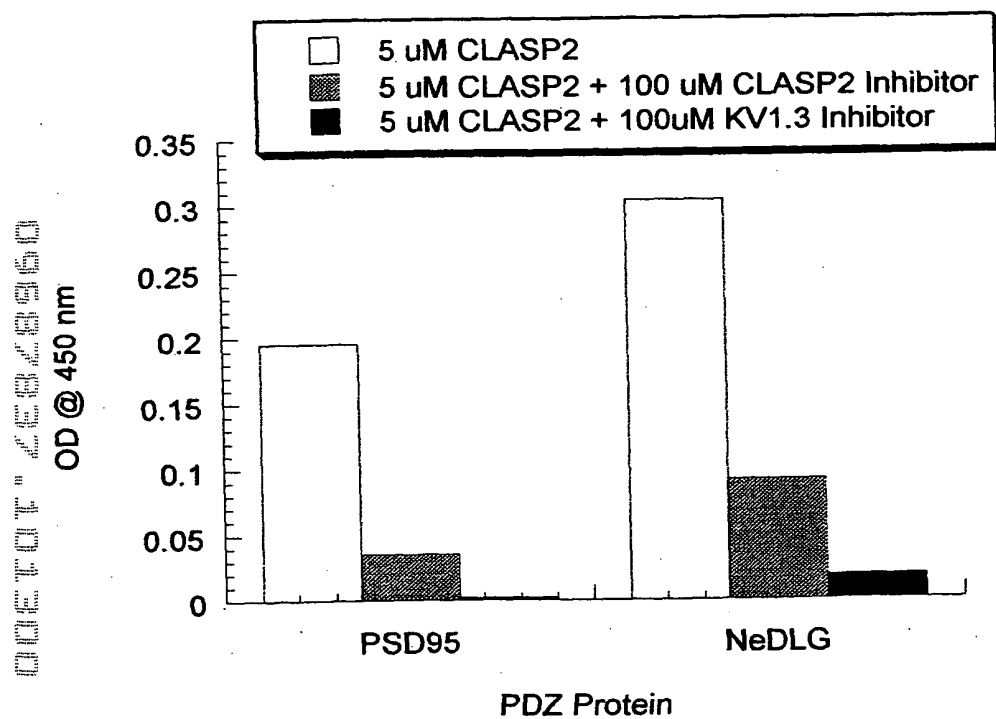


Fig. 9C

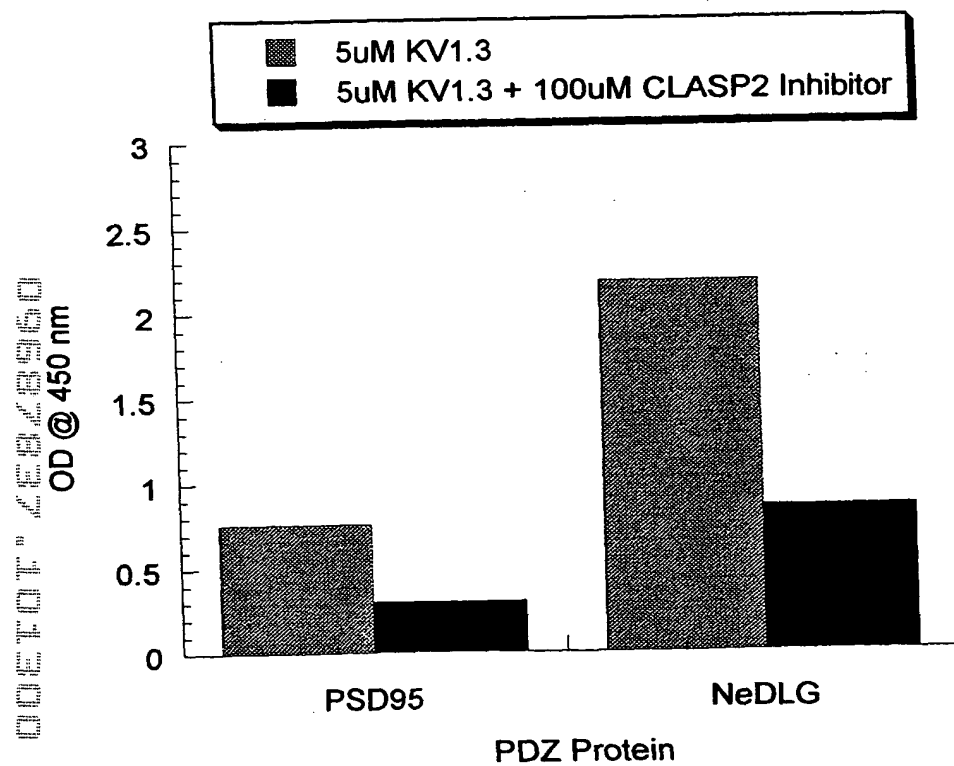


FIG. 9D

|      | 10          | 20          | 30          | 40          | 50          | 60          | 70         | 80          |
|------|-------------|-------------|-------------|-------------|-------------|-------------|------------|-------------|
| 1    | AATTGTAATA  | CGACTCACTA  | TAGGGCGAAT  | TGGGTACCGG  | GCCCCCCTC   | GAGGTCGACG  | GTATCGATAA | GCTTGATATC  |
| 81   | GAATTTCGGCA | CGAGTITTTAC | ACCATCACCA  | AAACCCAGAA  | TTTTATGATG  | AGATTAAAT   | AGAGTTGCC  | ACTCAGCTGC  |
| 161  | ATGAAAAGCA  | CCACCTGTTG  | CTCACATTCT  | TCCATGTGAG  | CTGTGACAAC  | TCAAGTAAAG  | GAAGCACGAA | GAAGAGGGAT  |
| 241  | GTGTTGAAA   | CCCAAGTTGG  | CTACTCTCTG  | CTTCCCCCTC  | TGAAAGACGG  | AAGGGTGGTG  | ACAAGCGAGC | AGCACATCCC  |
| 321  | GGTCTCGCG   | AACCTTCCTT  | CGGGCTATCT  | TGGCTACCAA  | GAGCTTGGGA  | TGGGCAGGCA  | TTATGGTCCG | GAAATTAAT   |
| 401  | GGGTAGATGG  | AGGCAAGCCA  | CTGCTGAAAA  | TTTCCACTCA  | TCTGGTTTCT  | ACAGGGATAC  | TCAGGATCAG | CAITTTACATA |
| 481  | ATTTTTTCCA  | GTACTGTGAG  | AAAACCGAAT  | CTGGAGCCCA  | AGCCTTAGGA  | AACGAACTTG  | TAAAGTACCT | TAAGAGTCTG  |
| 561  | CATGCGATGG  | AAGGCCACGT  | GATGATCGCC  | TTCTTGCCCA  | CTATCCTAAA  | CCAGCTGTTT  | CGAGTCTCTA | CCAGAGCCAC  |
| 641  | ACAGGAAGAA  | GTCGCGGTTA  | ACGTGACTCG  | GGTCATTATT  | CATGTGGTTG  | CCCAGTGCCA  | TGAGGAAGGA | TTGGAGAGCC  |
| 721  | ACTTGAGGTC  | ATATGTTAAG  | TACGCGTATA  | AGGCTGAGCC  | ATATGTTGCC  | TCTGAATACA  | AGACAGTGCA | TGAAGAACTG  |
| 801  | ACCAAATCCA  | TGACCACGAT  | TCTCAAGCCT  | TCTGCCGATT  | TCCTCACCAG  | CAACAACTTA  | CTGAGGTACT | CATGGTTTTT  |
| 881  | CTTTGATGTA  | CTGATCAAAT  | CTATGGCTCA  | GCATTITGATA | GAGAACTCCA  | AAGTTAAGTT  | GCTGCGAAAC | CAGAGATTTC  |
| 961  | CTGCATCCTA  | TCATCATGCA  | GCGGAAACCG  | TTGTAAATAT  | GCTGATGCCA  | CACATCACTC  | AGAAGTTTGG | AGATAATCCA  |
| 1041 | GAGGCATCTA  | AGAACGCGAA  | TCTAGCCCTT  | GCTGTCTTCA  | TCAAGAGATG  | TTTCACCTTC  | ATGGACAGGG | GCTTTGTCTT  |
| 1121 | CAAGCAGATC  | AACAACCTACA | TTAGCTGTTT  | TGCTCTGGGA  | GACCCAAAGA  | CCCTCTTTGA  | ATACAAAGTT | GAITTTCTCC  |
| 1201 | GTGTAGTGTG  | CAACCATGAA  | CATTATATTC  | CGTTGAACTT  | ACCAATGCCA  | TTTGGAAAAG  | GCAGGATTCA | AAGATACCAA  |
| 1281 | GACCTCCAGC  | TTGACTACTC  | ATTAAACAGAT | GAGTTCTGCA  | GAAACCACTT  | CTTGGTGGGA  | CTGTTACTGA | GGGAGGTGGG  |
| 1361 | GACAGCCCTC  | CAGGAGTTCG  | GGGAGGTCCG  | TCTGATCGCC  | CATGTGTTGC  | TCAAGAACCT  | GCTGATAAAG | GATCTTTTGG  |
| 1441 | ATGACAGATA  | TGCTTCAAGG  | AGCCATCAGG  | CAAGGATAGC  | CACCCTCTAC  | CTGCCCTCTG  | TTGGTCTGCT | GATTGAAAAC  |
| 1521 | GTCACGCGGA  | TCAATGTGAG  | GGATGTGTCA  | CCCTTCCCTG  | TGAACGCGGG  | CATGACCGTG  | AAGGATGAAT | CCCTGGCTCT  |
| 1601 | ACCAGCTGTG  | AATCCGCTGG  | TGACGCGCA   | GAAGGGAAGC  | ACCTTGGA    | ACAGCTTGCA  | CAAGGACCTG | CTGGGCGCCA  |
| 1681 | TCTCGCGCAT  | TGCTTCTCCA  | TATACAACCT  | CAACTCCAAA  | CATCAACAGT  | GTGAGAAATG  | CTGATTTCAG | AGGATCTCTC  |
| 1761 | ATAAGCACAG  | ATTCCGGTAA  | CAGCCTTCCA  | GAAAGGAATA  | GTGAGAAAGAG | CAATTCCCTG  | GATAAGCACC | AACAAGTAG   |
| 1841 | CACATTGGGA  | AATTCCTGGG  | TTGCTGTGTA  | TAAACTTGAC  | CAGTCTGAGA  | TTAAGAGCCT  | ACTGATGTGT | TTCTCTTACA  |
| 1921 | TCTTAAAGAG  | CATGCTGTAT  | GATGCTTTGT  | TTACATATTG  | GAACAAGGCT  | TCAACATCTG  | AACTTATGGA | TTTTTTTACA  |
| 2001 | ATATCTGAAG  | TCTGCCTGCA  | CCAGTTCAG   | TACATGGGGA  | AGCGATACAT  | AGCCAGGAAC  | CAGGAGGGGT | TGGGACCCAT  |
| 2081 | AGTTTCATGAT | CGAAGTCTC   | AGACATTGCC  | TGTTTCCCGT  | AACGAAACAG  | GAATGATGCA  | TGCCAGATTG | CAGGCTGGG   |
| 2161 | GCAAGCTGGA  | TAACCTCTCT  | ACTTTTAAAC  | ACAGCTATGG  | CCACTCGGAC  | GCAGATGTTT  | TGCACCAGTC | ATTACTTGAA  |
| 2241 | GCCAAACATT  | CTACTGAGGT  | TTGCCCTGACA | GCTCTGGACA  | CGCTTTCTCT  | ATTTTACATT  | GCGTTTAAAG | ACCAGCTCTT  |
| 2321 | GGCCGACCAT  | GGACATAATC  | CTCTCATGAA  | AAAAGTTTTT  | GATGTCTACC  | TGTGTTTTCT  | TCAAAAACAT | CAGCTGTGAA  |
| 2401 | CGGCTTTAAA  | AAATGTCTTC  | ACTGCCCTTA  | GGTCCCTAAT  | TTATAAGTTT  | CCCTCAACAT  | TCTATGAAGG | GAGAGCGGAC  |
| 2481 | ATGTGTGCGG  | CTCTGTGTTA  | CGAGATTCTC  | AAGTGTGTTA  | ACTCCAAGCT  | GAGCTCCATC  | AGGACGGAGG | CCTCCCAGCT  |
| 2561 | GCTCTACTTC  | CTGATGAGGA  | ACAACTTTGA  | TTACATGGGA  | AAGAAGTCTT  | TGTCTCGGAC  | ACATTTGCAA | GCTCATCAT   |
| 2641 | CTGTGAGCCA  | GCTGATAGCA  | GACGTTGTTG  | GCATTGGGGA  | AACCAGATTTC | CAGCAGTCCC  | TGTCCATCAT | CAACAACCTG  |
| 2721 | GCCAAACAGT  | ACCGGCTTAT  | TAAGCACACC  | AGCTTCTCCT  | CTGATGTGAA  | GGACTTAACC  | AAAAGGATAC | GCACGGTCTT  |
| 2801 | AATGGCCACC  | GCCCAGATGA  | AGGAGCATGA  | GAACGACCCA  | GAGATGCTGG  | TGGACCTCCA  | GTACAGCCTG | GCCAAATCCT  |
| 2881 | ATGCCAGCAC  | GCCCGAGCTC  | AGGAAGACGT  | GGCTCGACAG  | CATGGCCAGG  | ATCCATGTCA  | AAAATGGCGA | TCTCTCAGAG  |
| 2961 | GCAAGCAATG  | GCTATGTCCA  | CGTAACAGCC  | CTAGTGGCAG  | AATATCTCAC  | ACGGAAAGGC  | GTGTTTAGAC | AAGGATGCAC  |
| 3041 | CGCCTTCAGG  | GTCAATTACCC | CAAAACATCGA | CGAGGAGGCC  | TCCATGATGG  | AAGACGTGGG  | GATGCAGGAT | GTCCATTCCA  |
| 3121 | ACGAGGATGT  | GCTGATGGAG  | CTCCTTGAGC  | AGTGCCGAGA  | TGGAATCTGG  | AAAGCCGAGC  | GCTACGAGCT | CATCGCCGAC  |
| 3201 | ATCTACAAAC  | TTATCATCCC  | CATTATGAG   | AAGCGGAGGG  | ATTTCTTTGA  | AGATGAAGAT  | GGAAAGGAGT | ATATTTACAA  |
| 3281 | GGAACCCAAA  | CTCACACCGC  | TGTCGGAAT   | TTCTCAGAGA  | CTCCTTAAAC  | TGTACTCGGA  | TAAATTGGT  | TCTGAAAATG  |
| 3361 | TCAAAATGAT  | ACAGGATTCT  | GGCAAGGTCA  | ACCCTAAGGA  | TCTGGATTCT  | AAGTATGCAT  | ACATCCAGGT | GACTCACGTC  |
| 3441 | ATCCCTTCT   | TTGACGAAAA  | AGAGTTGCAA  | GAAAGGAAAA  | CAGAGTTTGA  | GAGATCCCAC  | AAACATCCGC | GCTTCATGTT  |
| 3521 | TGAGATGCCA  | TTTACGCAGA  | CCGGGAAGAG  | GCAGGGCGGG  | GTGGAAGAGC  | AGTGCAAAAC  | GCGCACCATC | CTGACAGCCA  |
| 3601 | TACACTGCTT  | CCCTTATGTG  | AAGAAGCGCA  | TCCCTGTCTAT | GTACCAGCAC  | CACACTGACC  | TGAACCCCAT | CGAGGTGGCC  |
| 3681 | ATTGACGAGA  | TGAGTAAGAA  | GGTGGCGGAG  | CTCCGCGCAG  | TGTGCTCCTC  | GGCCGAGGTG  | GACATGATCA | AACTGCAGCT  |
| 3761 | CAAACTCCAG  | GGCAGCGTGA  | GTGTTCAAGT  | CAATGCTGGC  | CCAATAGCAT  | ATGCGCGAGC  | TTTCTTAGAT | GATACAAACA  |
| 3841 | CAAAGCGATA  | TCTTGACAAT  | AAAGTGAAGC  | TGCTTAAAGGA | AGTTTTTCAGG | CAATTTGTGG  | AAGCTTGGCG | TCAAGCCTTA  |
| 3921 | CGGTAACAG   | AACGTCTGAT  | TAAAGAAGAC  | CAGCTCGAGT  | ATCAGGAAGA  | AATGAAAGCC  | AACTACAGGG | AAATGGCGAA  |
| 4001 | GGAGCTTTCT  | GAAATCATGC  | ATGAGCAGAT  | CTGCCCTCTG  | GAGGAGAAGA  | CGAGCGTCTT  | ACCGAATTCC | CTTCACATCT  |
| 4081 | TCAACGCCAT  | CAGTGGGACT  | CCAACAAGCA  | CAATGGTTCA  | CGGGATGACC  | AGCTCGTCTT  | CGGTGCTGTG | ATTACATCTC  |
| 4161 | ATGGCCCGTG  | TGTGGGGAGT  | TGCTTTGTCA  | TTTGCAAACT  | CAGGATGCTT  | TCCAAAGCCA  | ATCACTGGGG | AGACCGAGCA  |
| 4241 | CAGGGAGGAC  | CAAGGGGAGC  | GGGAGAGAAA  | GGAAATAAAG  | AACAACGTTA  | TTTCTTAAAC  | GACTTTCTAT | AGGAGTTGTA  |
| 4321 | AGAAGGTGCA  | CATATTTTTT  | TAAATCTCAC  | TGGCAATATT  | CAAAGTTTTT  | ATTGTGCTTT  | AACAAAGGTG | TGGTAGACAC  |
| 4401 | TCTTGAGCTG  | GACTTAGATT  | TTATCTTCC   | TTGCAGAGTA  | GTGTTAGAAT  | AGATGGCCTA  | CAGAAAAAAA | AGGTTCTGGG  |
| 4481 | ATCTACATGG  | CAGGGAGGGC  | TGCACTGACA  | TTGATCGCTG  | GGGAGCACTT  | TGCCCTCGACT | CGTGCCGGA  | ATCTGATCGT  |
| 4561 | AATCAGGGTA  | CAGAAGTTAC  | TAGTTTTGTC  | TAGGAGTATG  | TTGTATGACT  | AGGATTGTG   | CTATTATCTC | ATTCAACAAC  |
| 4641 | ATAGAGCAAG  | AATAGTGAGC  | TAACTGAGCT  | AGACACTCAA  | TTAATCCGCT  | ACTGGCTTCA  | AGTCAGAACT | TTGTCAATTA  |
| 4721 | TCATCGACTC  | CGGGACGGTC  | ATATATGTAT  | TACATTTCTA  | CTATTTTAA   | ACTCACATGG  | GCTTATGCAT | TAAGTTTAA   |
| 4801 | TGTGATAAAT  | TTGTGCTGCT  | CCAGTATATG  | CAATACACTT  | TAATGGTTTA  | TTCTGTGCTAT | AAAAATGTGC | AATATGGAGA  |
| 4881 | TGTATACAAG  | TCTTTACT    |             |             |             |             |            |             |

FIG. 10A

|      | 10          | 20          | 30          | 40          | 50         | 60          | 70          | 80              |
|------|-------------|-------------|-------------|-------------|------------|-------------|-------------|-----------------|
| 1    | MEGHVMIAFL  | PTILNQLFRV  | LTRATQEEVA  | VNVTRVIIHV  | VAQCHEEGLE | SHLRSYVKYA  | YKAEPYVASE  | YKTVHEELTK 80   |
| 81   | SMTILKPSA   | DFLTSNKLRL  | YSWFFFDVLI  | KSMAQH LIEN | SKVKLLRNQR | FPASYHHAAE  | TVVNMLMPHI  | TQKPGDNPEA 160  |
| 161  | SKNANHSLAV  | FIKRCFTFMD  | RGFVFKQINN  | YISCFAPGDP  | KTLFEYKFEF | LRVVCNHEHY  | IPLNLPMPFG  | KGRIQRYODL 240  |
| 241  | QLDYSLTDEF  | CRNHFLVGLL  | LREVGTAQOE  | FREVRLIAIS  | VLKNLLIKHS | FDDRYASRSH  | QARIATLYLP  | LFGLLIENVQ 320  |
| 321  | RINVRDVSPF  | PVNAGMTVKD  | ESLALPAVNP  | LVTPOKGSTL  | DNSLHKDLLG | AIISGIASPYT | TSTPNINSVR  | NADSRGSLIS 400  |
| 401  | TDSGNSLPER  | NSEKSNSLDK  | HQOSSTLGNS  | VVRCDKLDQS  | EIKSLLMCFL | YILKMSDDA   | LFTYWNKAST  | SELMDFFTIS 480  |
| 481  | EVCLHQFQYM  | GKRYIARNQE  | GLGPVHDKR   | SQTLPVSRNR  | TGMMHARLQQ | LGSLDNSLTF  | NHSYGHSDAD  | VLHQSLLEAN 560  |
| 561  | IATEVCLTAL  | DTLSLFTLAF  | KNOLLADHGH  | NPLMKKVFDV  | YLCFLOKHQS | ETALKNVFTA  | LRS LIYKFPS | TFYEGRADMC 640  |
| 641  | AALCYEILKC  | CNSKLSSIRT  | EASQLLYFLM  | RNNFDYTGKK  | SFVRTHLQVI | ISVSQLIADV  | VGIGETRFOQ  | SLSIINN CAN 720 |
| 721  | SDRLIKHTSF  | SSDVKDLTKR  | IRTVLMATAQ  | MKEHENDPEM  | LVDLQYSLAK | SYASTPELRK  | TWLD SMARIH | VKNGDLSEAA 800  |
| 801  | MCYVHV TALV | AEYLTRKGVF  | RQGC TAFRVI | TPNIDEEASM  | MEDVGMQDVH | FNEDVLMELL  | EQCADGLWKA  | ERYELIADIY 880  |
| 881  | KLIPIY EKR  | RDFFEDEDGK  | EYIYKEPKLT  | PLSEISQRLL  | KLYSDKFGSE | NVKMIQDSGK  | VNPKDLDSKY  | AYIQVTHVIP 960  |
| 961  | FFDEKELQER  | KTEFERSHNI  | RRFMFEMPFT  | QTGKRQGGVE  | EQCKRRTILT | AIHCFPYVKK  | RIPVMYQHHT  | DLNPIEVAID 1040 |
| 1041 | EMSKKVAELR  | QLCSSAEVDM  | IKLQLKLQGS  | VSVQVNAGPL  | AYARAFLDDT | NTKRYPDNKV  | KLLKEVFRQF  | VEACGQALAV 1120 |
| 1121 | NERLIKEDQL  | EYQEE MKANY | REMAKELSEI  | MHEQICPLEE  | KTSVLPNSLH | IFNAISGTPT  | STMVHGMTSS  | SSVV 1194       |

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FIG. 10A (cont.)

|      | 10          | 20          | 30         | 40          | 50          | 60          | 70         | 80          |
|------|-------------|-------------|------------|-------------|-------------|-------------|------------|-------------|
| 1    | AATTGTAATA  | CGACTCACTA  | TAGGGCGAAT | TGGGTACCGG  | GCCCCCCTC   | GAGGTGACG   | GTATCGATAA | GCTTGATATC  |
| 81   | GAATTCGGCA  | CGAGTTTITAC | ACCATCACCA | AAACCCAGAA  | TTTTATGATG  | AGATTAAAT   | AGAGTTGCC  | ACTCAGCTGC  |
| 161  | ATGAAAAGCA  | CCACCTGTTG  | CTCACATTCT | TCCATGTCAG  | CTGTGACAAC  | TCAAGTAAAG  | GAAGCACGAA | GAAGAGGGAT  |
| 241  | GTCTGTGAAA  | CCCAAGTTGG  | CTACTCCTGG | CTTCCCCTCC  | TGAAAGACGG  | AAGGGTGGTG  | ACAAGCGAGC | AGCACATCCC  |
| 321  | GGTCTCGGCG  | AACCTTCCCT  | CGGGCTATCT | TGGCTACCAA  | GAGCTTGGGA  | TGGGCAGGCA  | TTATGGTCCG | GAAATTTAAAT |
| 401  | GGGTAGATGG  | AGGCAAGCCA  | CTGCTGAAAA | TTTCCACTCA  | TCTGGTTTCT  | ACAGGGATAC  | TCAGGATCAG | CATTTACATA  |
| 481  | ATTTTTTCCA  | GTACTGTGAG  | AAAACCGAAT | CTGGAGCCCA  | AGCCTTAGGA  | AACGAACCTG  | TAAAGTACCT | TAAGAGTCTG  |
| 561  | CATGCGATGG  | AAGGCCACGT  | GATGATCGCC | TCTTCCCA    | CTATCCTAAA  | CCAGCTGTTT  | CGAGTCTCTA | CCAGAGCCAC  |
| 641  | ACAGGAAGAA  | GTGCGGGTTA  | ACGTGACTCG | GGTCAATTAT  | CATGTGGTTG  | CCCAGTGCCA  | TCTGAATACA | TGAGGAAGGA  |
| 721  | ACTTGAGGTC  | ATATGTTAAG  | TACGGGTATA | AGGCTGAGCC  | ATATGTTGCC  | TCTGAATACA  | AGACAGTGCA | TGAAGAACTG  |
| 801  | ACCAAAATCCA | TGACCACGAT  | TCTCAAGCCT | TCTGCCGATT  | TCCTCACCAG  | CAACAACTA   | CTGAGGTACT | CATGGTTTTT  |
| 881  | CTTTGATGTA  | CTGATCAAT   | CTATGGCTCA | GCATTTGATA  | GAGAACTCCA  | AAGTTAAGTT  | GCTGCGAAAC | CAGGAATTTT  |
| 961  | CTGCATCCTA  | TCATCATGCA  | GCGGAAACCG | TTGTAATAT   | CTGATGATCA  | CACATCACTC  | AGAAGTTTGG | AGATAATCCA  |
| 1041 | GAGGCATCTA  | AGAACGCGAA  | TCATAGCCTT | GCTGCTTTCA  | TCAAGAGATG  | TTTCACTTTC  | ATGGACAGGG | GCTTTGCTTT  |
| 1121 | CAAGCAGATC  | AACAACTACA  | TTAGCTGTTT | TGCTCCTGGA  | GACCCAAAGA  | CCCTCTTGA   | ATACAAGTTT | GAATTTCTTC  |
| 1201 | GTGTAGTGTG  | CAACCATGAA  | CATTATATTC | CGTTGAACCT  | ACCAATGCTT  | TTTGGAAAAG  | GCAGGATTCA | AAGATACCAA  |
| 1281 | GACCTCCAGC  | TTGACTACTC  | ATTAACAGAT | GAGTTCTGCA  | GAAACCACTT  | CTTGGTGGGA  | CTGTTACTGA | GGGAGGTGGG  |
| 1361 | GACAGCCCTC  | CAGGAGTTCC  | GGGAGGTCCG | TCTGATCGCC  | ATCAGTGTGC  | TCAAGAACCT  | GCTGATAAAG | CATTCTTTTG  |
| 1441 | ATGCAGATA   | TGCTTCAAGG  | AGCCATCAGG | CAAGGATAGC  | CACCTCTTAC  | CTGCCCTGCT  | TTGGTCTGCT | GATTGAAAAC  |
| 1521 | GTCCAGCGGA  | TCAATGTGAG  | GGATGTGTCA | CCCTTCCCTG  | TGAAACGCGG  | CATGACCGTG  | AAGGATGAAT | CCCTGGCTCT  |
| 1601 | ACCAGCTGTG  | AATCCGCTGG  | TGACGCGCGA | GAAGGGAAGC  | ACCCTTGACA  | ACAGCCTGCA  | CAAGGACCTG | CTGGGCGCCA  |
| 1681 | TCTCCGGCAT  | TGCTTCTCCA  | TATACAACCT | CAACTCCAAA  | CTCAACAGT   | GTGAGAAATG  | CTGATTGAG  | AGGATCTCTC  |
| 1761 | ATAAGCACAG  | ATTCCGGTAA  | CAGCCTTCCA | GAAAGGAATA  | GTGAGAAAGT  | CAATTCCCTG  | GATAAGCACC | AACAAGTAG   |
| 1841 | CACATTGGGA  | AATTCCGTGG  | TTCGCTGTGA | TAAACTTGAC  | CAGTCTGAGA  | TTAAGAGCCT  | ACTGATGTGT | TCTCTCTACA  |
| 1921 | TCTTAAAGAG  | CATGTCTGAT  | GATGCTTTGT | TTACATATTG  | GAACAAGGCT  | TCAACATCTG  | AACCTTATGA | TTTTTTTACA  |
| 2001 | ATATCTGAAG  | TCTGCCGTGA  | CCAGTCCAGG | TACATGGGGA  | AGCGATACAT  | AGCCAGGAAC  | CAGGAGGGGT | TGGGACCCAT  |
| 2081 | AGTTCATGAT  | CGAAAGTCTC  | AGACATTGCC | TGTTTCCCGT  | AACAGAACAG  | GAATGATGCA  | TGCCAGATTG | CGCAGCTGG   |
| 2161 | GCAGCCTGGA  | TAACTCTCTC  | ACTTTTAACT | ACAGCTATGG  | CCACTCGGAC  | GCAGATGTTT  | TGCACCACTG | ATTACTTGAA  |
| 2241 | GCCAACTATG  | CTACTGAGGT  | TGCGCTGACA | GCTCTGGACA  | CGCTTCTCTT  | ATTTACATTG  | CGGTTTAAAG | ACCAGCTCCT  |
| 2321 | GGCCGACCAT  | GGACATAATC  | CTCTCATGAA | AAAAGTTTTT  | GATGTCTTAC  | TGTGTTTTCT  | TCAAAAACAT | CAGCTGAAAT  |
| 2401 | CGGCTTTAAA  | AATGTCTTTC  | ACTGCCITAA | GGTCTTAAAT  | TTATAGCTTT  | CCCTCAACAT  | TCTATGAAGG | GAGAGCGGAC  |
| 2481 | ATGTGTGCGG  | CTCTGTGTTA  | CGAGATTCTC | AAGTGTCTGA  | ACTCCAAGCT  | GAGCTCCATC  | AGGACGGAGG | CCCTCCAGCT  |
| 2561 | GCTCTACTTC  | CTGATGAGGA  | ACAACCTTGA | TTACACTGGA  | AAGAAGTCTT  | TTGTCCGGAC  | ACATTTGCAA | GTCATCATAT  |
| 2641 | CTGTACGCCA  | CGTATAGCA   | GACGTTGTTG | GCATTGGGGA  | AACAGATATC  | CAGCAGTCCC  | TGTCCATCAT | CAACAACCTG  |
| 2721 | GCCAAACAGT  | ACCGGCTTAT  | TAAACACACC | AGCTTCTCCT  | CTGATGTGAA  | GGACTTAAAC  | AAAAGGATAC | GCACGGTCTT  |
| 2801 | AATGCCACCC  | GCCCGAGTGA  | AGGAGCATGA | GAACGACCCA  | GAGATGCTGG  | TGGACCTCCA  | GTACAGCCTG | GCCAAATCCT  |
| 2881 | ATGCCAGCAC  | GCCCGAGCTC  | AGGAAGACGT | GGCTCGACAG  | CATGGCCAGG  | ATCCATGTGA  | AAAATGGCGA | TCTCTCAGAG  |
| 2961 | GCAGCAATGT  | GCTATGTCCA  | CTTAACAGCC | CTAGTGGCAG  | AATATCTTAC  | ACCGAAAGGC  | GTGTTTAGAC | AAGGATGCA   |
| 3041 | CGCCTTCAGG  | GTCAATTACC  | CAAACATCGA | CGAGGAGGCC  | TCCATGATGG  | AAGAGCTGGG  | GATGCAAGAT | GTCATTCTCA  |
| 3121 | ACGAGGATGT  | GCTGATGGAG  | CTCCTTGAGC | AGTGGCGAGA  | TGGACTCTGG  | AAAGCCGAGC  | GCTACGAGCT | CATCGCCGAC  |
| 3201 | ATCTACAAAC  | TTATCATCCC  | CATTTATGAG | AAGCGGAGGG  | ATTTCTTTGA  | AGATGAAGAT  | GGAAAGGAGT | ATATTTACAA  |
| 3281 | GGAAACCCAA  | CTCACACCGC  | TGTCGGAAAT | TTCTCAGAGA  | CTCCTTAAAC  | TGTACTCGGA  | TAAATTTGGT | TCTGAAAATG  |
| 3361 | TCAAAATGAT  | ACAGGATTCT  | GGCAAGGTCA | ACCCTAAGGA  | TCTGGATTCT  | AAGTATGCA   | ACATCCAGGT | GACTCACGTC  |
| 3441 | ATCCCCCTCT  | TTGACGAAAA  | AGAGTTGCAA | GAAAGGAAAA  | CAGAGTTTGA  | GAGATCCCA   | AACATCCGCC | GCTTCATGTT  |
| 3521 | TGAGATGCCA  | TTTACGCGAA  | CCGGGAAGAG | GCAGGGCGGG  | GTGGAAGAGC  | AGTGCAAAAC  | GCGCACCATC | CTGACAGCCA  |
| 3601 | TACACTGCTT  | CCCTTATGTT  | AAGAAGCGCA | TCCCTGTCTAT | GTACCAGCAC  | CACACTGACC  | TGAACCCCAT | CGAGGTGGCC  |
| 3681 | ATTGACGAGA  | TGAGTAAGAA  | GGTGGCGGAG | TCCCGGCAGC  | TGTGCTCCTC  | GGCCGAGGTC  | GACATGATCA | AACATGACCT  |
| 3761 | CAAACTCCAG  | GGCAGCGTGA  | GTGTTTCAGT | CAATGCTGGC  | CCACTAGCAT  | ATGCGCGAGC  | TTTCTTAGAT | GATACAAACA  |
| 3841 | CAAAGCGATA  | TCTGACAAAT  | AAAGTGAAGC | TGCTTAAAGG  | AGTTTTTCAGG | CAATTGTGGG  | AAGCTTGGCG | TCAAGCCTTA  |
| 3921 | GCGGTAAACG  | AACGTCTGAT  | TAAAGAAGAC | CAGCTCGAGT  | ATCAGGAAGA  | AATGAAAGCC  | AACTACAGGG | AAATGGCGAA  |
| 4001 | GGAGCTTTCT  | GAAATCATGC  | ATGAGCAGAT | CTGCCCCCTG  | GAGGAGAAGA  | CGAGCGTCTT  | ACCGAATTCC | CTTCACTCT   |
| 4081 | TCAACGCCAT  | CAGTGGGACT  | CCAACAAGCA | CAATGGTTCA  | CGGGATGACC  | AGCTCGTCTT  | CGGTGCTGTG | ATTACATCTC  |
| 4161 | ATGGCCCGTG  | TGTGGGGACT  | TGCTTTGTCA | TTTGCAAACT  | CAGGATGCTT  | TCCAAAGCCA  | ATCACTGGGG | AGACCGAGCA  |
| 4241 | CAGGAGGAGC  | CAAGGGGAAG  | GGGAGAGAAA | GGAAATAAAG  | AACAACGTTA  | TTTCTTAAAC  | GACTTTCTAT | AGGAGTTGTA  |
| 4321 | AGAAGGTGCA  | CATATTTTTT  | TAAATCTCAC | TGGCAATATT  | CAGAGTTTTC  | ATTGTGTCTT  | AACAAAGGTC | TGGTAGACAC  |
| 4401 | TCTTGAGCTG  | GACTTAGATT  | TTATTCTTCC | TTGCAGAGTA  | GTGTTAGAAT  | AGATGGCCTA  | CAGAAAAAAA | AGGTTCTGGG  |
| 4481 | ATCTACATGG  | CAGGAGGGGC  | TGCACTGACA | TTGATGCCTG  | GGGGACCTTT  | TGCCTCGACT  | CGTGCCGGAA | ACTGATCGT   |
| 4561 | AATCAGGGTA  | CAGAACTTAC  | TAGTTTTGTC | TAGGAGTATG  | TTGATGACT   | AGGATTTGTG  | CTATTATCTC | ATTCAACAAC  |
| 4641 | ATAGAGCAAG  | AATAGTGAGC  | TAACTGAGCT | AGACACTCAA  | TTAATCCGCT  | ACTGGCTTCA  | AGTCAGAACT | TTGTCAATTA  |
| 4721 | TCATCGACTC  | CGGAGCGGTC  | ATATATGTAT | TACATTTCTA  | CATTTTTAAT  | ACTCACATGG  | GCTTATGCAT | TAAGTTTAAAT |
| 4801 | TGTGATAAAT  | TTGTCTGGT   | CCAGTATATG | CAATACACTT  | TAATGGTTTA  | TTCTGTGCTAT | AAAAATGTGC | AATATGGAGA  |
| 4881 | TGTATACAAG  | TCCTTACT    |            |             |             |             |            |             |
|      | 10          | 20          | 30         | 40          | 50          | 60          | 70         | 80          |
|      |             |             |            |             |             |             |            | 4898        |



|      | 10          | 20          | 30          | 40          | 50         | 60         | 70          | 80              |
|------|-------------|-------------|-------------|-------------|------------|------------|-------------|-----------------|
| 1    | MEGHVMI AFL | PTILNQLFRV  | LTRATQEEVA  | VNVTRV I HV | VAQCHEEGLE | SHLRSYVKYA | YKAEPYVASE  | YKTVHEELTK 80   |
| 81   | SMTTILKPSA  | DFLTSNKL LR | YSWFFFDVLI  | KSMAOHLIEN  | SKVKLLRNQR | FPASYHHAAE | TVVNMIMPHI  | TQKFGDNPEA 160  |
| 161  | SKNANHSLAV  | FIKRCFTFMD  | RGFVFKQINN  | YISCFAPGDP  | KTLFEYKFEF | LRVVCNHEHY | IPLNLPMPFG  | KGRIQRYODL 240  |
| 241  | QLDYSLTDEF  | CRNHFLVGLL  | LREVGTLAQE  | FREVRLIAIS  | VLKNLLIKHS | FDDRYASRSH | QARIATLYLP  | LPGLLIENVQ 320  |
| 321  | RINVRDVSPF  | PVNAGMTVKD  | ESLALPAVNP  | LVTPOKGSTL  | DNSLHKDLLG | AISGIASPYT | TSTPNINSVR  | NADSRGSLIS 400  |
| 401  | TDSGNSLPER  | NSEKSNSLDK  | HQOSSTLGNS  | VVRCDKLDQS  | EIKSLLMCFL | YILKSMDDA  | LFTYWNKAST  | SELMDFFTIS 480  |
| 481  | EVCLHQFOYM  | GKRYIARNQE  | GLGPIVHDRK  | SQTLFVSRNR  | TGMMHARLQQ | LGSLDNSLTF | NHSYGHSDAD  | VLHQSLLEAN 560  |
| 561  | IATEVCLTAL  | DTLSLFTLAF  | KNQLLADHGH  | NPLMKKVFDV  | YLCFLQKHQS | ETALKNVFTA | LRSLIYKFPS  | TFYEGRADMC 640  |
| 641  | AALCYEILKC  | CNSKLSSTRT  | EASQLLYFLM  | RNNFDYTGKK  | SFVRTHLQVI | ISVSQLIADV | VGIGETRFOQ  | SLSIINNCAN 720  |
| 721  | SDRLIKHTSF  | SSDVKDLTKR  | IRTVLMATAQ  | MKEHENDPEM  | LVDLQYSLAK | SYASTPELRK | TWLD SMARIH | VKNGDLSEAA 800  |
| 801  | MCYVHV TALV | AEYLTRKGVF  | RQGCTAFRVI  | TPNIDEEASM  | MEDVGMQDVH | FNEDVLMELL | EQCADGLWKA  | ERYELIADIY 880  |
| 881  | KLIIPITYEKR | RDFFEDEDGK  | EYIYKEPKLT  | PLSEISQRLI  | KLYSDKPGSE | NVKMIQDSGK | VNPKOLD SKY | AYIQVTHVIP 960  |
| 961  | FFDEKELQER  | KTEFERSHNI  | RRFMPFEMPFT | QTGKRQGGVE  | EQCKRRTILT | AIHCFFPYVK | RIPVMYQHHT  | DLNPIEVAID 1040 |
| 1041 | EMSKKVAELR  | QLCSSAEVDM  | IKLQKLQGS   | VSVQVNA GPL | AYARAFLDDT | NTKRYPDNKV | KLLKEVFRQF  | VEACQALAV 1120  |
| 1121 | NERLIKEDQL  | EYQEEMKANY  | REMAKELSEI  | MHEQICPLEE  | KTSVLPNSLH | IFNAISGTPT | STMVHGMTSS  | SSVV 1194       |

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FIG. 1DB (cont.)

|    |             |             |            |             |             |             |            |             |
|----|-------------|-------------|------------|-------------|-------------|-------------|------------|-------------|
|    | 10          | 20          | 30         | 40          | 50          | 60          | 70         | 80          |
| 1  | AATTGTAATA  | CGACTCACTA  | TAGGGCGAAT | TGGGTACCGG  | GCCCCCCTC   | GAGGTGACG   | GTATCGATAA | GCTTGATATC  |
| 2  | GAATTCGGCA  | CGAGTTTTTAC | ACCATCACCA | AAACCCAGAA  | TTTTATGATG  | AGATTAAAT   | AGAGTTGCC  | ACTCAGCTGC  |
| 3  | ATGAARAAGCA | CCACCTGTG   | CTCACATTCT | TCCATGTCAG  | CTGTGACAAC  | TCAAGTAAAG  | GAAGCAGGAA | GAAGAGGGAT  |
| 4  | GTCGTTGAAA  | CCCAAGTTGG  | CTACTCCTGG | CTTCCCTCC   | TGAAGAAGCGG | AAGGGTGGTG  | ACAAGCGAGC | AGCACATCCC  |
| 5  | GGTCTCGGCG  | AACTTCTCTT  | CGGGCTATCT | TGGCTACCAA  | GAGCTTGGGA  | TGGGCAGGCA  | TTATGGTCCG | GAAATTAAT   |
| 6  | GGGTAGATGG  | AGGCAAGCCA  | CTGCTGAAAA | TTTCCACTCA  | TCTGGTTTTCT | ACAGGGATAC  | TCAGGATCAG | CATTTACATA  |
| 7  | ATTTTTTCCA  | GTACTGTCTAG | AAAACCGAAT | CTGGAGCCCA  | AGCCTTAGGA  | AACGAACITG  | TAAAGTACCT | TAAGAGTCTG  |
| 8  | CATGCGATGG  | AAGGCCACGT  | GATGATCGCC | TTCTTGCCCA  | CTATCCTAAA  | CCAGCTGTTT  | CGAGTCTCTA | CCAGAGCCAC  |
| 9  | ACAGGAAGAA  | GTGCGGGTTA  | ACGTGACTCG | GGTCATTATT  | CATGTGGTTG  | CCCAGTGCCA  | TGAGGAAGGA | TTGGAGAGCC  |
| 10 | ACTTGAGGTC  | ATATGTTAAG  | TACGGGTATA | AGGCTGAGCC  | ATATGTTGCC  | TCTGAATACA  | AGACAGTGCA | TGAAGAAGCT  |
| 11 | ACCAAATCCA  | TGACCACGAT  | TCTCAAGCCT | TCTGCGGATT  | TCCTCACCAG  | CAACAACTA   | CTGAGGTACT | CATGGTTTTT  |
| 12 | CTTTGATGTA  | CTGATCAAAAT | CTATGGCTCA | GCATTTGATA  | GAGAACTCCA  | AAGTTAAGTT  | GCTGCGAAAC | CAGAGATTTC  |
| 13 | CTGCATCTCA  | TCAATCATGCA | GCGGAACCG  | TTGTAATATAT | GCTGATGCCA  | CACATCACTC  | AGAAGTTTGG | AGATAATCCA  |
| 14 | GAGGCATCTA  | AGAAACGCGAA | TCATAGCCCT | GCTGTCTTCA  | TCAAGAGATG  | TTTCACTTTC  | ATGGACAGGG | GCTTTGTCTT  |
| 15 | CAAGCAGATC  | AATCACTACA  | TTAGCTGTTT | TGCTCCTGGA  | GACCCAAAGA  | CCCTCTTGA   | ATACAAGTTT | GAATTTCTCC  |
| 16 | GTGTAGATGG  | CAACCTAGAA  | CATTATATTC | CGTTGAACCT  | ACCAATGCCA  | TTTGGAAAG   | GCAGGATTCA | AAGATACCAA  |
| 17 | GACCTCCAGC  | TTGACTACTC  | ATTAACAGAT | GAGTTCTGTA  | GAACCACTT   | CTTGGTGGGA  | CTGTTACTGA | GGGAGGTGGG  |
| 18 | GACAGCCCTC  | CAGGAGTTCC  | GGGAGGTCCG | TCTGATCGCC  | ATCAGATGTC  | TCAAGAACCT  | GCTGATAAAG | CATTCTTTTG  |
| 19 | ATGACAGATA  | TGCTTCAAGG  | AGCCATCAGG | CAAGGATAGC  | CACCTCTAC   | CTGCTCTGT   | TTGGTCTGCT | CCTTGAAAC   |
| 20 | GTCCAGCGGA  | TCAATGTGAG  | GATGTGTGCA | CCCTTCCCTG  | TGAACGCGGG  | CATGACCGTG  | AAGGATGAAT | CCCTGGCTCT  |
| 21 | ACCAGCTGTG  | AATCCCTGCG  | TGAAGCGGCA | GAAGGGAAGC  | ACCTTGGACA  | ACAGCCTGCA  | CAAGGACCTG | CTGGGCGCCA  |
| 22 | CTCCCGCAT   | TGCTTCTCCA  | TATACAACCT | CAACTCCAAA  | CATCAACAGT  | GTGAGAAATG  | CTGATTTCAG | AGGATCTCTC  |
| 23 | ATAAGCACAG  | ATTCCGGTAA  | CAGCCTTCCA | GAAAGGAATA  | GTGAGAAGAG  | CAATTTCCCTG | GATAAGCACC | AACAAAGTAG  |
| 24 | CACATTTGGG  | AATTCCTGAG  | TTGCTGTGTA | TAAACTTGAC  | CAGTCTGAGA  | TTAAGAGCCT  | ACTGATGTGT | TTCTCTTACA  |
| 25 | TCCTAAAGAG  | CATGCTGAT   | GATGCTTTGT | TTACATATTG  | GAACAAGGCT  | TCAACATCTG  | AACTTATGGA | TTTTTTTACA  |
| 26 | ATATCTGAAG  | TCTGCTGCA   | CCAGTTCCAG | TACATGGGGA  | AGCGATACAT  | AGCCAGGAAC  | CAGGAGGGGT | TGGGACCCAT  |
| 27 | AGTTCTGATG  | CGAAAGTCTC  | AGACATTGCC | TGTTTCCCGT  | AAACAGAACAG | GAATGATGCA  | TGCCAGATTG | CAGCAGCTGG  |
| 28 | GGAGCCTTGA  | TAACTCTCTC  | ACTTTTAACC | ACAGCTATGG  | CCACTCGGAC  | GCAGATGTTT  | TGCACCACTG | ATTACTTGAA  |
| 29 | GCCAACATTG  | CTACTGAGGT  | TTGCTTGACA | GCCTTGAGCA  | CGCTTCTCT   | ATTTACATTG  | GGGTTTAAAG | ACCAGCTCCT  |
| 30 | GGCCGACCAT  | GGACATAATG  | CTCTCATGAA | AAAAGTTTTT  | GATGTCTACC  | TGTGTTTTCT  | TCAAAAACAT | CAGTCTGAAA  |
| 31 | CGCTTTTAAA  | AAATGTCTTC  | ACTGCCCTAA | GGTCTTAAT   | TTATAAGTTT  | CCCTCAACAT  | TCTATGAAGG | GAGAGCGGAC  |
| 32 | ATGTGTGCGG  | CTCTGTGTTA  | CGAGATTCTC | AAGTGTGTTA  | ACTCCAAGCT  | GAGCTCCATC  | AGGACGGGAT | CCTCCAGCT   |
| 33 | GCTCTACTTC  | CTGATGAGGA  | ACAACCTTGA | TTACACTGGA  | AAGAAGTCTT  | TGTCCGGAC   | ACATTTGCAA | GTCTCATAT   |
| 34 | CTGTACGCCA  | GCTGATAGCA  | ACGTTGTTG  | GCATTGGGGA  | AAACAGATTG  | CAGCAGTCCC  | TGTCCATCAT | CAACAACCTG  |
| 35 | GCCAACAGTG  | ACCGGCTTAT  | TAGCACACC  | AGCTTCTCCT  | TCGATGTGAA  | GGACTTAAAC  | AAAAGGATAC | GCACGGTGCT  |
| 36 | AATGGCCACC  | GCCCGATGTA  | AGGAGCATGA | GAACGACCCA  | GAGATGTGAT  | TGGACCTCCA  | GTACAGCCTG | GCCAAATCCT  |
| 37 | ATGCCAGCAC  | GCCCGAGCTC  | AGGAAGACGT | GGCTCGACAG  | CATGGCCAGG  | ATCCATGTCA  | AAAATGGCGA | TCTCTCAGAG  |
| 38 | GCAGCAATGT  | GCTATGTCCA  | CGTAACAGCC | CGAGGAGGCC  | AATATCTCAC  | ACGGAAGGC   | GTGTTTAGAC | AAGGATGCAC  |
| 39 | CGCCTTCAGG  | GTCAATACCC  | CAACATCGA  | AGTGGCAGGA  | TCCATGTATG  | AAGACGTGGG  | GATGCAGGAT | GTCCATTTCA  |
| 40 | ACGAGGATGT  | GCTGATGGAG  | CTCCTTGAGC | TACCTCGAGT  | TGGACTCTGG  | AAAGCCGAGC  | GCTACGAGCT | CATCGCCGAC  |
| 41 | ATCTACAAC   | TTATCATCCC  | CATTTATGAG | AAGCGGAGGG  | ATTTCTTTGA  | AGATGAAGAT  | GGAAAGGAGT | ATATTTACAA  |
| 42 | GGAAACCCAA  | CTCACACCCG  | TGTCCGAAAT | TTCTCAGAGA  | CTCCTTAAAC  | TGTACTCGGA  | TAAATTTGGT | TCTGAAAATG  |
| 43 | TCAAAATGAT  | ACAGGATTCT  | GGCAAGGTCA | ACCCTAAGGA  | TCTGGATTCT  | CAGAGTTTGA  | AACATCCAGG | GACTCACGTC  |
| 44 | ATCCCTTCT   | TTGACGAAAA  | AGAGTTGCAA | GAAAGGAAAA  | CAGAGTTTGA  | GAGATCCCAT  | AACATCCGCC | GCTTCATGTT  |
| 45 | TGAGATGCCA  | TTTACGCGAG  | CCGGGAAGAG | GCAGGGCGGG  | GTGGAAGAGC  | AGTGCAAACG  | GCGCACCATC | CTGACAGCCA  |
| 46 | TACACTGCTT  | CCCTTATGTT  | AAGAAGCGCA | TCCCTGTCTAT | GTACCAGCAC  | CACACTGACC  | TGAACCCCAT | CGAGGTGGCC  |
| 47 | ATTGACGAGA  | TGAGTAAGAA  | GGTGGCGGAG | CTCCGGCAGC  | TGTGCTCTCT  | GGCCGAGGTG  | GACATGATCA | AACTGCAGCT  |
| 48 | CAAACTCCAG  | GGCAGCGTGA  | GTGTTCAAGT | CAATGCTGGC  | CCACTAGCAT  | ATGCGCGAGC  | TTTCTTAGAT | GATACAAACA  |
| 49 | CAAAGCGATA  | TCCTGACAAAT | AAAGTGAAGC | TGCTTAAAGG  | AGTTTTCAGG  | CAATTTGTGG  | AAGCTTGGCG | TCAAGCCTTA  |
| 50 | GCGGTAAACG  | AACGTCTGAT  | TAAAGAGAGC | CAGCTCGAGT  | ATCAGGAAGA  | AATGAAAGCC  | AACACAGGG  | AAATGGCGAA  |
| 51 | GAGCTTTTCT  | GAAATCATGC  | ATGAGCAGAT | CTGCCCTCTG  | GAGGAGAAGA  | CGAGCGTCTT  | ACCGAATTCC | CTTCACATCT  |
| 52 | TCAACGCCAT  | CAGTGGGACT  | CCAACAAGCA | CAATGGTTCA  | CGGGATGACC  | AGCTCGTCTT  | CGGTGCTGTG | ATTACATCTC  |
| 53 | ATGGCCCGTG  | TGTGGGGACT  | TGCTTTGTCA | TTTGCAAAC   | CAGGATGCTT  | TCCAAAGCCA  | ATCACTGGGG | AGACCGAGCA  |
| 54 | CAGGGAGGAG  | CAAGGGGAGG  | GGGAGAGAAA | GGAAATAAAG  | AACAACGTTA  | TTTCTTAAAC  | GACTTTCTAT | AGGAGTTGTA  |
| 55 | AGAAGGTGCA  | CATATTTTCT  | TAAATCTCAC | TGCAATATAT  | CAAAGTTTTC  | ATTGTGTCTT  | AACAAAGGTG | TGTTAGACAC  |
| 56 | TCTTGAGCTG  | GACTTAGATT  | TTATCTTCC  | TTGCAGAGTA  | GTGTTAGAAAT | AGATGGCCTA  | CAGAAAAAAA | AGGTTCTGGG  |
| 57 | ATCTACATGG  | CAGGGAGGGC  | TGCACGTACA | TTGATGCTCG  | GGGGACCTTT  | TGCTCGACT   | CGTCCCGGAA | ATCTGATCGT  |
| 58 | AATCAGGGTA  | CAGAATTAC   | TAGTTTGTG  | TAGGAGTATG  | TGTATGACT   | AGGATTTGTG  | CTATTATCTC | ATTCAACAAC  |
| 59 | ATAGAGCAAG  | AATAGTGAGC  | TAACGTAGCT | AGACACTCAA  | TTAATCCGCT  | ACTGGCTTCA  | AGTCAGAACT | TTGTCAATTA  |
| 60 | TCATCGACTC  | CGGACCGGTC  | ATATATGTAT | TACATTTCTA  | CATTTTAAAT  | ACTCACATGG  | GCTTATGCTC | TAAGTTTAAAT |
| 61 | TGTGATAAAT  | TTGTGCTGGT  | CCAGTATATG | CAATACACTT  | TAATGGTTTA  | TTCTGTCTAT  | AAAAATGTGC | AATATGGAGA  |
| 62 | TGTATACAG   | TCCTTACT    |            |             |             |             |            |             |
|    | 10          | 20          | 30         | 40          | 50          | 60          | 70         | 80          |

Fig. 10C

|   |            |            |            |            |            |            |             |                 |
|---|------------|------------|------------|------------|------------|------------|-------------|-----------------|
|   | 10         | 20         | 30         | 40         | 50         | 60         | 70          | 80              |
|   | MEGHVMI    | PTILNQLFRV | LTRATQEEVA | VNVTRVIIHV | VAQCHEEGLE | SHLRSYVKYA | YKAEFYVASE  | YKTVHEELTK 80   |
|   | SMITILKPSA | DFLTSNKLRL | YSWFFFDVLI | KSMAOHLIEN | SKVKLLRNQR | FPASYHHAEE | TVVMMLMPHI  | TQKPGDNPEA 160  |
|   | SKNANHSLAV | FIKRCFTFMD | RGFVFKQINN | YISCFAPGDP | KTLFEYKPEF | LRVVCNHEHY | IPINLPMPPG  | KGRIQRYQDL 240  |
|   | QLDYSLTDEF | CRNHFLVGLL | LREVGTAQOE | FREVRLLAIS | VJONLLIKHS | FDDRYASRSH | QARIATLYLP  | LPGLLIENVQ 320  |
|   | RINVRDVSPF | PVNAGMTVKD | ESLALPAVNP | LVTPOKGSTL | DNSLHKOLLG | AISGLASPTT | TSTPNINSVR  | NADSRGSLIS 400  |
| 1 | TDSGNSLPER | NSEKSNSLDK | HQOSSTLGNS | VVRCDKLDQS | EIKSLIMCFL | YILKSMDDA  | LFTYWNKAST  | SELMDFFTIS 480  |
| 1 | EVCLHQFOYM | GKRYIARNQE | GLGPIVHDRK | SOTLPVSRNR | TGMHARLOQ  | LGSLDNSLTF | NHSYGHSDAD  | VLHQSLLEAN 560  |
| 1 | IATEVCLTAL | DTLSLFTLAF | KNQLLADHGH | NPLMKKVFDV | YLCFLQKHQS | ETALKWFTA  | LRSLIYKPPS  | TFYEGRADMC 640  |
| 1 | AALCYEILKC | CNSKLSSTRT | EASQLLYFLM | RNNFDYTGKK | SFVRTHLQVI | ISVSQLIADV | VGIGETRPQQ  | SLSIINNAN 720   |
| 1 | SDRLIKHTSF | SSDVKDLTKR | IRTVLMATAQ | MKEHENDPEM | LVDLQYSLAK | SYASTPELRK | TWLDSEARH   | VKNGDLSEAA 800  |
| 1 | MCYVHVITLV | AEYLTRKGVF | ROGCTAFRVI | TPNIDEEASM | MEDVGMQDVH | FNEDVLMELL | EQCADGLMKA  | ERYELIADIY 880  |
| 1 | KLIPIYIEKR | RDPFEDEDGK | EYIYKEPKLT | PLSEISQRLI | KLYSDKFGSE | NVKMIQDSGK | VNPKDLDISKY | AYIQVTHVIP 960  |
| 1 | FFDEKELQER | KTEPERSHNI | RRFMFEMPPT | QTGKROGGVE | EQCKRRTILT | AIHCFPYVKK | RIPVMYQHHT  | DLNPIEVAID 1040 |
| 1 | EMSKVAELR  | QLCSSAEVDM | IKLQKLOGS  | VSVQVWAGPL | AYARAFDDT  | NTKRYPDNKV | KLLKEVFRQP  | VEACQALAV 1120  |
| 1 | NERLIKEDQL | EYOEMKANY  | REMAKELSEI | MHEQICPLEE | KTSVLNLSH  | IFNAISGTPT | STMVHGMITSS | SSVV 1194       |

Fig. 10C (cont.)

|      | 10          | 20          | 30          | 40          | 50          | 60         | 70          | 80          |
|------|-------------|-------------|-------------|-------------|-------------|------------|-------------|-------------|
| 1    | AATTGTAATA  | CGACTCACA   | TAGGGCGAAT  | TGGGTACCGG  | GCCCCCCCCT  | GAGGTGACG  | GTATCGATAA  | GCTTGATATC  |
| 81   | GAATTCGGCA  | CGAGTTTAC   | ACCATCACCA  | AAACCCAGAA  | TTTTATGATG  | AGATTAAAT  | AGAGTTGCC   | ACTCAGCTGC  |
| 61   | ATGAAAAGCA  | CCACCTGTTG  | CTCACCATTCT | TCCATGTCAG  | CTGTGACAAC  | TCAAGTAAAG | GAAGCACGAA  | GAAGAGGGAT  |
| 41   | GTGCTGAAA   | CCCAAGTTGG  | CTACTCCTGG  | CTTCCCTTCC  | TGAAAGACGG  | AAGGGTGGTG | ACAAGCCGAGC | AGCACATCCC  |
| 21   | GGTCTCGGCG  | AACCTTCCCT  | CGGGCTATCT  | TGGCTACCAA  | GAGCTTGGGA  | TGGGCAGGCA | TTATGGTCCG  | GAAATTAAT   |
| 01   | GGGTAGATGG  | AGGCAAGCCA  | CTGCTGAAAA  | TTTCCACTCA  | TCTGGTTTCT  | ACAGGGATAC | TCAGGATCAG  | CATTTACATA  |
| 81   | ATTTTTTCCA  | GTACTGTCAG  | AAAACCGAAT  | CTGGAGCCCA  | AGCCTTAGGA  | AACGAACCTG | TAAAGTACCT  | TAAGAGTCTG  |
| 61   | CATGCGATGG  | AAGGCCACGT  | GATGATCGCC  | TTCTTGCCCA  | CTATCCTAAA  | CCAGCTGTTT | CGAGTCCCTCA | CCAGAGCCAC  |
| 41   | ACAGGAAGAA  | GTCGCGGTTA  | ACGTGACTCG  | GGTCAATTATT | CATGTGGTGG  | CCCAGTGCCA | TGAGGAAGGA  | TTGGAGAGCC  |
| 21   | ACTTGAGGTC  | ATATGTTAAG  | TACGCGTATA  | AGGCTGAGCC  | ATATGTTGCC  | TCTGAATACA | AGACAGTGCA  | TGAAGAAGCTG |
| 801  | ACCAATCCCA  | TGACCAAGAT  | TCTCAAGCCT  | TCTGCGGATT  | TCCTCACCAG  | CAACAACTA  | CTGAGGTACT  | CATGGTTTTT  |
| 881  | CTTTGATGTA  | CTGATCAAAAT | CTATGGCTCA  | GCATTGTGATA | GAGAACTCCA  | AAGTTAAGTT | GCTGCGAAAC  | CAGAGATTTC  |
| 961  | CTGCATCTCA  | TCAATCATGCA | CGGGAACCG   | TTGTAATATT  | GCTGATGCCA  | CACATCACTC | AGAAGTTTGG  | AGATAATCCA  |
| 041  | GAGGCATCTA  | AGAAACGGAA  | TCATAGCCTT  | GCTGTCTTCA  | TCAAGAGATG  | TTTCACTTTC | ATGGACAGGG  | GCTTTGTCTT  |
| 121  | CAAGCAGATC  | AACAACATCA  | TTAGCTGTTT  | TGCTCCTGGA  | GACCCAAAG   | CCCTCTTGA  | ATACAAGTTT  | GAATTTCTCC  |
| 201  | GTGTATGTG   | CAACCATGAA  | CATTATATT   | CGTTGAACTT  | ACCAATGCCA  | TTTGGAAAG  | GCAGGATTCA  | AGATACATA   |
| 281  | GACCTCCAGC  | TTGACTACTC  | ATTACAGAT   | GAGTTCTGCA  | GAACCACTT   | CTTGGTGGGA | CTGTTACTGA  | GGGAGGTGGG  |
| 1361 | GACAGCCCTC  | CAGGAGTTCC  | GGGAGGTCCG  | TCTGATCGCC  | ATCAGTGTGC  | TCAAGAACCT | GCTGATAAAG  | CATTCTTTTG  |
| 1441 | ATGACAGATG  | TGCTTCAAGG  | AGGCATCAGG  | CAAGGATGAC  | CACCTCTAC   | CTGCCCTGT  | TTGGTCTGCT  | GATTGAAAC   |
| 1521 | GTCCAGCGGA  | TCAATGTGAG  | GGATGTGTCA  | CCCTTCCCTG  | TGAAGCGCGG  | CATGACCGTG | AAGGATGAAT  | CCCTGGCTCT  |
| 1601 | ACCAGCTGTG  | AATCCGCTGG  | TGAAGCGGCA  | GAAGGGAAGC  | ACCCCTGGACA | ACAGCCTGCA | CAAGGACCTG  | CTGGGCGCCA  |
| 1681 | TCTCCGGCAT  | TGCTTCTCCA  | TATACAACCT  | CAACTCCAAA  | CATCAACAGT  | GTGAGAAATG | CTGATTGAG   | AGGATCTCTC  |
| 1761 | ATAAGCACAG  | ATTCCGGTAA  | CAGCCTTCCA  | GAAAGGAATA  | GCTGAGAAGAG | CAATTCCTTG | GATAAGCACC  | AACAAAGTAG  |
| 1841 | CACATTGGGA  | AATTCGCTGG  | GTGCTGTGTA  | TAACTTTGAC  | CATGCTGAGA  | TTAAGAGCCT | ACTGATGTGT  | TTCTCTTACA  |
| 1921 | TCTTAAAGAG  | CATGCTGTAT  | GATGCTTTGT  | TACATATTG   | GAACAAGGCT  | TCAACATCTG | AACCTTATGGA | TTTTTTTACA  |
| 2001 | ATATCTGAAG  | TCTGCTGCA   | CCAGTTCCAG  | TACATGGGGA  | AGCGATACAT  | AGCCAGGAAC | CAGGAGGGGT  | TGGGACCCAT  |
| 2081 | AGTTCTATGAT | CGAAAGTCTC  | AGACATTGCC  | TGTTTCCCGT  | AACAGATCAG  | GAATGATGCA | TGCCAGATTG  | CAGCAGCTGG  |
| 2161 | GCAGCCTGGA  | TAACTCTCTC  | ACTTTTAAAC  | ACAGCTATGG  | CCACTCGGAC  | GCAGATGTTT | TGCACCATG   | ATTACTTGAA  |
| 2241 | GCCAACATTG  | CTACTGAGGT  | TGCTTGACA   | GCTCTGGACA  | CGCTTCTCT   | ATTACATTTG | CGGTTTAAAG  | ACCAGCTCCT  |
| 2321 | GGCCGACCAT  | GGACATAATC  | CTCTCATGAA  | AAAAGTTTTT  | GATGCTTACC  | TGTGTTTTCT | TCAAAAACAT  | CAGTCTGAAA  |
| 2401 | GGCTTTTAAA  | AAATGTCTTC  | ACTGCCITAA  | GGTCTTAAT   | TTATAAGTTT  | CCCTCAACAT | TCTATGAAGG  | GAGAGCGGAC  |
| 2481 | ATGTGTGCGG  | CTCTGTGTTA  | AGATGCTCTC  | AAGTGTCTGA  | ACTCCAAGCT  | GAGCTCCATC | AGGACGGAGG  | CTCCAGCT    |
| 2561 | GCTCTACTTC  | CTGATGAGGA  | ACAACCTTGA  | TTACACTGGA  | AAGAAGTCC   | TTGTCCGGAC | ACATTTGCAA  | GTCTCATAT   |
| 2641 | GTGTGAGCCA  | CGTGTAGCA   | GACGTTGTTG  | GCATTTGGGA  | AAACAGATT   | CAGCAGTCCC | TGTCCATCAT  | CAACAACGT   |
| 2721 | GCCAACAGTG  | ACCGGCTTAT  | TAAGCACACC  | AGCTTCTCCT  | CTGATGTGAA  | GGACTTAAAC | AAAAGGATAC  | GCCAAATCCT  |
| 2801 | AATGGCCACC  | GCCCGATGTA  | AGGAGCATGA  | GAACGACCCA  | GAGATGTGAG  | TGGACCTCCA | GTACAGCCTG  | GCTTCTCAGG  |
| 2881 | ATGCCAGCAC  | GCCCGAGCTC  | AGGAAGACGT  | GGCTCGACAG  | CATGGCCAGG  | ATCCATGTCA | AAAATGGCGA  | TTCTCTCAGG  |
| 2961 | GCAGCAATGT  | GCTATGTCCA  | CGTAACAGCC  | CTAGTGGCAG  | AATATCTCAC  | ACGAAAGGC  | GTGTTTAGAC  | AAGGATGCAC  |
| 3041 | CGCCTTCAGG  | GTCAATACCC  | CAACATCGA   | CGAGGAGGCC  | TCCATGTAGG  | AAGACGTGGG | GATGCAAGAT  | GTCCATTTCA  |
| 3121 | ACGAGGATGT  | GCTGATGGAG  | CTCCTTGAGC  | AGTGCAGAGA  | TGGACTCTGG  | AAAGCCGAGC | GCTACGAGCT  | CATGCCGAC   |
| 3201 | ATCTACAAC   | TTATCATCCC  | CATTATGAG   | AAGCCGAGGG  | ATTTCTTTGA  | AGATGAAGAT | GGAAAGGAGT  | ATATTTACAA  |
| 3281 | GGAAACCAAA  | CTCACACCGC  | TGTCCGAAAT  | TTCTCAGAGA  | CTCCTTAAAC  | TGTACTCGGA | TAAATTTGGT  | TCTGAAAATG  |
| 3361 | TCAAAATGAT  | ACAGGATTCT  | GCCAAGGTCA  | ACCCTAAGGA  | TCTGGATTCT  | AAGTATGCAT | ACATCCAGGT  | GACTCACGTC  |
| 3441 | ATCCCTTTCT  | TTGACGAAAA  | AGAGTTGCAA  | GAAAGGAAAA  | CAGAGTTTGA  | GAGATCCAC  | AACATCCGCC  | GCTTCATGTT  |
| 3521 | TGAGATGCCA  | TTTACGCGA   | CCGGGAAGAG  | GCAGGGCGGG  | GTGGAAGAGC  | AGTGCAAACG | GCGCAACCAT  | CTGACAGCCA  |
| 3601 | TACACTGCTT  | CCCTTATGTG  | AAGAAGCGCA  | TCCCTGTCTAT | GTACCAGCAC  | CACACTGACC | TGAACCCCAT  | CGAGGTGGCC  |
| 3681 | ATTGACGAGA  | TGAGTAAGAA  | GGTGGCGGAG  | CTCCGGCAGC  | TGTGCTCCTC  | GGCCGAGGTG | GACATGATCA  | AACCTGAGCT  |
| 3761 | CAAACTCCAG  | GGCAGCGTGA  | GTGTTCAAGT  | CAATGCTGGC  | CCACTAGCAT  | ATCCGCGAGC | TTTCTTAGAT  | GATACAAACA  |
| 3841 | CAAAGCGATA  | TCCTGACAAT  | AAAGTGAAGC  | TGCTTAAAGGA | AGTTTTTCAGG | CAATTTGTGG | AAGCTTGGCG  | TCAAGCCTTA  |
| 3921 | GCGGTAACG   | AACGTCTGAT  | TAAAGAGAC   | CAGCTCGAGT  | ATCAGGAAGA  | AATGAAGCC  | AACCAAGGG   | AAATGGCGAA  |
| 4001 | GGAGCTTTCT  | GAAATCATGC  | ATGAGCAGAT  | CTGCCCTCTG  | GAGGAGAAGA  | CGAGCGTCTT | ACCGAATTCC  | CTTACATCT   |
| 4081 | TCAACGCCAT  | CAGTGGAGCT  | CCAACAAGCA  | CAATGGTTCA  | CGGGATGACC  | AGCTCGTCTT | CGGTGCTGTG  | ATTACATCTC  |
| 4161 | ATGGCCCGTG  | TGTGGGACT   | TGCTTTGTCA  | TTTGCAAACT  | CAGGATGCTT  | TCCAAAGCCA | ATCACTGGGG  | AGACCGAGCA  |
| 4241 | CAGGGAGGAC  | CAAGGGGAAG  | GGGAGAGAAA  | GGAATAAAG   | AACAACGTTA  | TTTCTTAAAC | GACTTTCTAT  | AGGAGTTGTA  |
| 4321 | AGAAGGTGCA  | CATATTTTTT  | TAAATCTCAC  | TGGCAATATT  | CAAAGTTTTT  | ATTGTGTCTT | AACAAAGGTG  | TGGTAGACAC  |
| 4401 | TCTTGAGCTG  | GACTTAGATT  | TTATTTCTCC  | TTGCAGAGTA  | GTGTTAGATT  | AGATGGCCTA | CAGAAAAAAA  | AGGTTCTGGG  |
| 4481 | ATCTACATGG  | CAGGGAGGGC  | TGCACTGACA  | TTGATGCCCTG | GGGGACCTTT  | TGCCCTGACT | CGTGCCGGAA  | ATCTGATCGT  |
| 4561 | AATCAGGGTA  | CAGAACTTAC  | TAGTTTTGTC  | TAGGAGTAGT  | TTGTATGACT  | AGGATTGTG  | CTATTATCTC  | ATTCAACAAC  |
| 4641 | ATAGAGCAAG  | AATAGTGAGC  | TAACGTAGCT  | AGACACTCAA  | TTAATCCGCT  | ACTGGCTTCA | AGTCAGAACT  | TTGTCAATTAA |
| 4721 | TCATCGACTC  | CGGACCGGTC  | ATATATGTAT  | TACATTTCTA  | CATTTTTAAT  | ACTCAGATGG | GCTTATGCA   | TAAGTTTAAAT |
| 4801 | TGTGATAAAT  | TTGTGCTGGT  | CCAGTATATG  | CAATACACTT  | TAATGGTTTA  | TTCTGTGAT  | AAAAATGTGC  | AAATATGGAGA |
| 4881 | TGTATACAG   | TCTTTACT    |             |             |             |            |             |             |
|      | 10          | 20          | 30          | 40          | 50          | 60         | 70          | 80          |

Fig. 10D

|    | 10         | 20          | 30         | 40         | 50         | 60         | 70          | 80              |
|----|------------|-------------|------------|------------|------------|------------|-------------|-----------------|
|    | MEGHVMAFL  | PTILNQLFRV  | LTRATQEEVA | VNVTRVHHV  | VAQCHEEGLE | SHLRSYVKA  | YKAEPYVASE  | YKTVHEELTK 80   |
|    | SMITILKPSA | DFLTSTNKLAR | YSWFFFDVLI | KSMACHLIEN | SKVKLLRNQR | FPASYHHAEE | TVVNMMPHI   | TQKFGDNPEA 160  |
|    | SKNANHSLAV | FIKRCFTFMD  | RGFVFKQINN | YISCFAPGDP | KTLFEYKFEF | LRVVCNHEHY | IPINLPMPPG  | KGRIQRYQDL 240  |
|    | QLDYSLTDEF | CRNHFLVGLL  | LREVGTLAQE | FREVRLLAIS | VLFNLLIKHS | FDDRYASRSH | QARIATLYLP  | LPGLLIENVO 320  |
|    | RINVRDVSPF | PVNAGMTVKD  | ESLALPAVNP | LVTPOKGSTL | DNSLHKDLLG | AISGIASPYT | TSTFNINSVR  | NADSRGSLIS 400  |
| 1  | TDGNSLPER  | NSEKSNSLDK  | HQSSSTLGNS | VVRCDKLDQS | EIKSLIMCFL | YILKMSDDA  | LFTYWNKAST  | SELMOFFTIS 480  |
| 1  | EVCLHQFOYM | GKRYIARNOE  | GLGPIVHDKR | SQTLPVSRNR | TGMMHARLQQ | LGSIDNSLTF | NHSYGHSDAD  | VLHQSLLEAN 560  |
| 1  | IATEVCLTAL | DTLSLFTLAF  | KNQLLADHGH | NPLMKKVFDV | YLCFLQKHQS | ETALQNVFTA | LRSIYKFPS   | TFYEGRADMC 640  |
| 1  | AALCYEILKC | CNSKLSIRT   | EASQLLYFLM | RNNFDYTGKX | SFVRTHLQVI | ISVSQLIADV | VGIGETRPQQ  | SLSIINNCAN 720  |
| 1  | SDRLIKHTSF | SSDVKDLTKR  | IRTVLMATAQ | MKEHENDPEM | LVDLQYSLAK | SYASTPELRK | TWLDSEMARH  | VWGDLESEA 800   |
| 1  | MCYVHVTALV | AEYLTRKGVF  | ROGCTAFRVI | TPNIDEEASM | MEDVGMQDVH | FNEDVLMELL | EQCADGLWKA  | ERYELIADTY 880  |
| 1  | KLIPIYKCR  | RDFFEDDGK   | EYIYKEPKLT | PLSEISQRLI | KLYSDKFGSE | NVKMIQDSGK | VNPKDLDISKY | AYIQVTHVIP 960  |
| 51 | FFDEKELQER | KTEFERSHNI  | RRFMPFMPPT | QTGKRQGGVE | EQCKRTILT  | AIHCFFPVVK | RIPVMYQHHT  | DLNPIEVAID 1040 |
| 41 | EMSKKVAELR | QLCSEAEDVM  | IKLQKLQGS  | VSVQVAGPL  | AYARAFLLDT | NTKRYPDNKV | KLLKEVFRQF  | VEACQALAV 1120  |
| 21 | NERLIKEDOL | EYQEEMKANY  | REMAKELSEI | MHEQICPLEE | KTSVLPNSLH | IFNAISGTYT | STMVHGMTSS  | SSV 1194        |

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FIG. 10D (CONT.)

|             |             |             |             |             |             |            |             |
|-------------|-------------|-------------|-------------|-------------|-------------|------------|-------------|
| 10          | 20          | 30          | 40          | 50          | 60          | 70         | 80          |
| AATTGTAATA  | CGACTCACTA  | TAGGGCGAAT  | TGGGTACGGG  | GCCCCCCCCC  | GAGGTGACAG  | GTATCGATAA | GCTTGATATC  |
| GAATTTCGGCA | CGAGTTTAC   | ACCATCACCA  | AAACCCAGAA  | TTTTATGATG  | AGATTAAAAAT | AGAGTTGCC  | ACTCAGCTGC  |
| ATGAAAAGCA  | CCACCTGTTG  | CTCACATTCT  | TCCATGTCAG  | CTGTGACAAAC | TCAAGTAAAG  | GAAGCACGAA | GAAGAGGGAT  |
| GTCTGTGAAA  | CCCAAGTTGG  | CTACTCCTGG  | CTTCCCCCTCC | TGAAAGACGG  | AAGGGTGGTG  | ACAAGCGAGC | AGCACATCCC  |
| GGTCTCGGGG  | AACTTTCCTT  | CGGGCTATCT  | TGGCTACCAA  | GAGCTTGGGA  | TGGGCAAGCA  | TTATGGTCCG | GAAATTTAAAT |
| GGGTAGATGG  | AGGCAAGCCA  | CTGCTGAAAA  | TTTCCACTCA  | TCTGGTTTCT  | ACAGGGATAC  | TCAGGATCAG | CATTTACATA  |
| ATTTTTTTCCA | GTACTGTTCAG | AAAACCGAAT  | CTGGAGCCCA  | AGCCTTAGGA  | AACGAACCTG  | TAAAGTACCT | TAAAGTCTG   |
| CATGCGATGG  | AAGCCACGT   | GATGATCGCC  | TTCTTGCCCA  | CTATCCTAAA  | CCAGCTGTTT  | CGAGTCTCTA | CCAGAGCCAC  |
| ACAGGAAGAA  | GTGCGGTTA   | ACGTGACTCG  | GGTCAATTAT  | CATGTGGTGG  | CCCAGTGCCA  | TGAGGAAGGA | TTGGAGAGCC  |
| ACTTGAGGTC  | ATATGTTAAG  | TACGCGTATA  | AGGCTGAGCC  | ATATGTTGCC  | TCTGAATACA  | AGACAGTGCA | TGAAGAACTG  |
| ACCAAATCCA  | TGACCAAGAT  | TCTCAAGCCT  | TCTGCGGATT  | TCCTCACCAG  | CAACAACTA   | CTGAGGTACT | CATGGTTTTT  |
| CTTTGATGTA  | CTGATCAAAAT | CTATGGCTCA  | GCAATTGATA  | GAGAACTCCA  | AAGTTAAGTT  | GCTGCGAAAC | CAGAGATTTT  |
| CTGCATCCTA  | TCATCATGCA  | GCGGAAACCG  | TTGTAATAT   | GCTGATGCCA  | CACATCACTC  | AGAAGTTTGG | AGATAATCCA  |
| GAGGCATCTA  | AGAAACGCGAA | TCATAGCCTT  | GCTGTCTTCA  | TCAAGAGATG  | TTTCACTTTC  | ATGGACAGGG | GCTTTGTCTT  |
| CAAGCAGATC  | AACAACCTA   | TTAGCTGTTT  | TGCTCCTGGA  | GACCCAAAGA  | CCCTCTTGA   | ATACAAGTTT | AAGATACCAA  |
| GTGTATGTTG  | CAACCATGAA  | CATTATATTC  | GGTTGAACCT  | ACCAATGCCA  | TTTGAAAAAG  | GCAGGATTC  | GGGAGGTGGG  |
| GACCTCCAGC  | TTGACTACTC  | ATTAACAGAT  | GAGTTCTGCA  | GAAACCACTT  | CTTGTGGGA   | CTGTTACTGA | CATTCTTTT   |
| GACAGCCCTC  | CAGGAGTTCC  | GGGAGGTCCG  | TCTGATGGCC  | ATCAGTGTGC  | TCAAGAACCT  | GCTGATAAAG | GATTGAAAAC  |
| ATGACAGATA  | TGCTTCAAGG  | AGCCTCAGG   | CAAGGATAGC  | CACCCCTCTAC | CTGCCCTCTG  | TTGGTCTGCT | CCCTGGCTCT  |
| GTCCAGCGGA  | TCAATGTGAG  | GGATGTGTCA  | CCCTTCCCTG  | TGAAACGCGG  | CATGACCGTG  | AAGGATGAAT | CTGGGCGCCA  |
| ACCAGCTGTG  | AATCCGCTGG  | TGACGCGCGA  | GAAGGGAAGC  | ACCCGTGACA  | ACAGCCTGCA  | CAAGGACCTG | CTGGGCGCCA  |
| TTCCCGGCAT  | TGCTTCTCCA  | TATACAACCT  | CAACTCCAAA  | CATCAACAGT  | GTGAGAAATG  | CTGATTTCAG | AGGATCTCTC  |
| ATAAGCACAG  | ATTCCGGTTA  | CAGCCTTCCA  | GAAAGGAATA  | GTGAGAAGAG  | CAATTCCTCT  | GATAAGCACC | AACAAAGTAG  |
| CACATTGGGA  | AATTCCGTTG  | TTCCGTGTGA  | TAAACTTGAC  | CAGTCTGAGA  | TTAAGAGCCT  | ACTGATGTGT | TTCTCTTACA  |
| TCCTAAAGAG  | CATGCTGTAT  | GATGCTTTGT  | TTACATATTG  | GAACAAGGCT  | TCAACATCTG  | AACCTTATGA | TTCTCTTACA  |
| ATATCTGAAG  | TCTGCTGTCA  | CCAGTTCCAG  | TACATGGGA   | AGCGATACAT  | AGCCAGGAAC  | CAGGAGGGGT | TGGGACCCAT  |
| AGTTCTATGAT | CGAAAGTCTC  | AGACATTGCC  | TGTTTCCCGT  | AAACAGAACG  | GAATGATGCA  | TGCCAGATTG | CAGCAGCTGG  |
| GCAGCTGGA   | TAACTCTCTC  | ACTTTTAAAC  | ACAGCTATGG  | CCACTCGGAC  | GCAGATGTTT  | TGCCAGATTG | CAGCAGCTGG  |
| GCCACATTTG  | CTACTGAGGT  | TTGCCCTGACA | GCTCTGGACA  | CGCTTTCTCT  | ATTTACATTG  | GGGTTTAAAG | ACCAGCTCCT  |
| GGCGGACCAT  | GGACATAATC  | CTCTCATGAA  | AAAAGTTTTT  | GATGTCTACC  | TGTGTTTTCT  | TCAAAAACAT | CAGTCTGAAA  |
| CGGCTTTAAA  | AAATGCTCTC  | ACTGCCCTTAA | GGTCTTAAAT  | TTATAAGTTT  | CCCTCAACAT  | TCTATGAAGG | GAGAGCGGAC  |
| ATGCTGTGCG  | CTCTGTGTTA  | CGAGATTCTC  | AAGTGTCTGA  | ACTCCAAGCT  | GAGCTCCATC  | AGGAACGGAG | CCTCCAGCT   |
| GCTCTACTTC  | CTGATGAGGA  | ACAACTTTGA  | TTACATGGA   | AAGAAGCCTT  | TTGTCCGGAC  | ACATTTTGCA | GTCTCATAT   |
| CTGTGAGCCA  | GCTGATAGCA  | GACGTGTGTG  | GCATTGGGGA  | AACCAGATTC  | CAGCAGTCCC  | TGTCCATCAT | CAACAACTGT  |
| GGCAACATGT  | AGCGGCTTAT  | TAAGCACACC  | AGCTTCTCCT  | CTGATGTGAA  | GGACTTAACC  | AAAAGGATAC | GCACGGTCT   |
| AAATGCCACC  | GCCCAGATGA  | AGGAGCATGA  | GAACGACCCA  | GAGATGTCTG  | TGGACCTCCA  | GTACAGCCTG | GCCAAATCTT  |
| ATGECAGCAC  | GCCCGAGCTC  | AGGAAGAGCT  | GGCTCGACAG  | CATGGCCAGG  | ATCCATGTCA  | AAAATGGGGA | TCTCTCAGAG  |
| GGCACAATGT  | GCTATGTCCA  | CGTAACAGCC  | CTAGTGCCAG  | AATATCTCAC  | ACGGAAAGGC  | GTGTTTAGAC | AAGGATGCCAC |
| CGCCTTCAGG  | GTCAATTACCC | CAAACATCGA  | CGAGGAGGCC  | TCCATGATGG  | AAGACGTGGG  | GATGCAGGAT | GTCTATTCTA  |
| ACGAGGATGT  | GCTGATGGAG  | CTCCTTGAGC  | AGTGCCGAGA  | TGGACTCTGG  | AAAGCCGAGC  | GCTACGAGCT | CATCCGCGAC  |
| ATTTACAAAC  | TTATCATCCC  | CATTTATGAG  | ANGCCGAGGG  | ATTTCTTTGA  | AGATGAAGAT  | GGAAAGGAGT | ATATTTACAA  |
| GGAAACCAAA  | CTCACACCGC  | TGTCCGAAAT  | TTCTCAGAGA  | CTCCTTAAAC  | TGTACTCGGA  | TAAATTTGGT | TCTGAAAATG  |
| TCAAAATGAT  | ACAGGATTCT  | GGCAAGGTCA  | ACCCTAAGGA  | TCTGGATTCT  | AAGTATGCAT  | ACATCCAGGT | GACTCACGTC  |
| ATCCCCCTCT  | TTGACGAAAA  | AGAGTTGCAA  | GAAAGGAAAA  | CAGAGTTTGA  | GAGATCCAC   | AACATCCGCC | GCTTCATGTT  |
| TTAGATGCCA  | TTTACGCAGA  | CCGGGAAGAG  | GCAGGGGCGG  | GTGGAAGAGC  | AGTGCAAAAG  | GCGCACCATC | CTGACAGCCA  |
| TGACTGTCTT  | CCCTTATGTG  | AAGAAGCGCA  | TCCCTGTCTAT | GTACCAGCAC  | CACACTGACC  | TGAACCCCAT | CGAGGTGGCC  |
| ATTGACGAGA  | TGAGTAAGAA  | GGTGGCGGAG  | CTCCGGCAGC  | TGTGCTCCTC  | GGCCGAGGTG  | GACATGATCA | GATACAAACA  |
| CAAACTCCAG  | GGCAGGTGA   | GTGTTCAAGT  | CAATGCTGGC  | CCACTAGCAT  | ATGCGCGAGC  | TTTCTTAGAT | TCAAGCCTTA  |
| CAAAGCGATA  | TCTTGACAAT  | AAAGTGAAGC  | TGCTTAAAGCA | AGTTTTTCAGG | CAATTTGTGG  | AAGCTTGCGG | AAATGGCGAA  |
| GGGTAAAGCG  | AACGCTGTAT  | TAAAGAAGAC  | CAGCTCGAGT  | ATCAGGAAGA  | AATGAAAGCC  | AACACAGGG  | AAATGGCGAA  |
| GGAGCTTTCT  | GAAATCATGC  | ATGAGCAGAT  | CTGCCCTCTG  | GAGGAGAAGA  | CGAGCTCTT   | ACCGAATTCC | CTTCACATCT  |
| TCAACGCCAT  | CAGTGGGACT  | CCAACAAGCA  | CAATGGTTCA  | CGGGATGACC  | AGCTCGTCTT  | CGGTCGTGTG | ATTACATCTC  |
| ATGGCCCGTG  | TGTGGGGAAT  | TGCTTTGTCA  | TTTGCAAACT  | CAGGATGCTT  | TCCAAAGCCA  | ATCACTGGGG | AGACCGAGCA  |
| CAGGGAGGAC  | CAAGGGGAAG  | GGGAGAGAAA  | GGAAATAAAG  | AACAACGTTA  | TTTCTTAAAC  | GACTTTCTAT | AGGAGTTGTA  |
| AGAAGGTGCA  | CATATTTTTT  | TAAATCTCAC  | TGGCAATATT  | CAAAGTTTTT  | ATTTGTCTTT  | AACAAAGGTG | TGGTAGACAC  |
| TCTTGAGCTG  | GACTTAGATT  | TTATTTCTTC  | TTGCAGAGTA  | GTGTTAGAAT  | AGATGGCCTA  | CAGAAAAAAA | AGGTTCTGGG  |
| ATCTACATGG  | CAGGAGGGGC  | TGCACGTACA  | TTGATGCTTG  | GGGACCTTTT  | TGCCCTGACT  | CGTGCGGGAA | ATCTGATCGT  |
| AATCAGGGTA  | CAGAACTTAC  | TAGTTTTGTC  | TAGGAGTATG  | TTGTATGACT  | AGGATTTGTG  | CTATTATCTC | ATTCAACAAAC |
| ATAGAGCAAG  | AATAGTGAGC  | TAACTGAGCT  | AGACACTCAA  | TTAATCCGCT  | ACTGGCTTCA  | AGTCAGAACT | TTGTCAATTAA |
| TCATCGACTC  | CGGAGCGGTC  | ATATATGTAT  | TACATTTCTA  | CATTTTTAAT  | ACTCACATGG  | GCTTATGCAT | TAAGTTTAAAT |
| TGTGATAAAT  | TTGTGCTGGT  | CCAGTATATG  | CAATACACTT  | TAATGGTTTA  | TTCTTGTCAT  | AAAAATGTGC | AATATGGAGA  |
| TGTATACAG   | TCITTACT    |             |             |             |             |            |             |
| 10          | 20          | 30          | 40          | 50          | 60          | 70         | 80          |

Fig. 10E



|             | 10          | 20         | 30          | 40         | 50          | 60          | 70          | 80   |
|-------------|-------------|------------|-------------|------------|-------------|-------------|-------------|------|
| AATTGTAATA  | CGACTCACTA  | TAGGGCGAAT | TGGGTACCGG  | GCCCCCCCCC | GAGGTGACGG  | GTATCGATAA  | GCTTGATATC  | 80   |
| GAATTCGGCA  | CGAGTTTAC   | ACCATCACCA | AAACCAGAA   | TTTTATGATG | AGATTAAAAT  | AGAGTTGCC   | ACTCAGCTGC  | 160  |
| ATGAAAAGCA  | CCACCTGTG   | CTCACATTCT | TCCATGTCAG  | CTGTGACAAC | TCAAGTAAAG  | GAAGCACGAA  | GAAGAGGGAT  | 240  |
| GTCGTTGAAA  | AACAAGTTGG  | CTACTCCTGG | CTTCCCTCC   | TGAAAGACGG | AAGGGTGGTG  | ACAAGCGAGC  | AGCACATCCC  | 320  |
| GGTCTCGGCG  | AACCTTCTCT  | CGGGCTATCT | TGGCTACCAA  | GAGCTTGGGA | TGGGACGGCA  | TTATGGTCCG  | GAAATTAAT   | 400  |
| GGGTAGATGG  | AGGCAAGCCA  | CTGCTGAAAA | TTTCCACTCA  | TCTGGTTTCT | ACAGGGATAC  | TCAGGATCAG  | CATTTACATA  | 480  |
| ATTTTITCCA  | GTACTGTCTAG | AAAACCGAAT | CTGGAGCCCA  | AGCCTTAGGA | AACGAACTTG  | TAAAGTACCT  | TAAGAGTCTG  | 560  |
| CATGCCGATG  | AAGGCCACGT  | GATGATCGCC | TTCTTGCCCA  | CTATCCTAAA | CCAGCTGTTC  | CGAGTCCCTCA | CCAGAGCCAC  | 640  |
| ACAGGAAGAA  | GTCGCGGTTA  | ACGTGACTCG | GGTCATTATT  | CATGTGGTTG | CCCAGTGCCA  | TGAGGAAGGA  | TTGGAGAGCC  | 720  |
| ACTTGAGGTC  | ATATGTTAAG  | TACGCGTATA | AGGCTGAGCC  | ATATGTTGCC | TCTGAATACA  | AGACAGTGCA  | TGAAGAACTG  | 800  |
| ACCAAATCCA  | TGACCACGAT  | TCTCAGCCT  | TCTGCCGATT  | TCCTCACCAG | CAACAACTA   | CTGAGGTACT  | CATGGTTTTT  | 880  |
| CTTTGATGTA  | CTGATCAAA   | CTATGGCTCA | GCATTTGATA  | GAGAATCTCA | AAGTTAAGTT  | GCTGCGAAAC  | CAGAGATTTT  | 960  |
| CTGCATCCTA  | TCATCATGCA  | GCGGAAACCG | TTGTAAATAT  | GCTGATGCCA | CACATCACTC  | AGAAGTTTGG  | AGATATATCCA | 1040 |
| GAGGCACTCA  | AGAAACGCGAA | TCATAGCCTT | GCTGTCTTCA  | TCAGAGATG  | TTTCACTTTC  | ATGGACAGGG  | GCTTTGTCTT  | 1120 |
| CAAGCAGATC  | AACAACCTA   | TTAGCTGTTT | TGCTCCTGGA  | GACCCAAAGA | CCCTCTTGA   | ATACAAGTTT  | GAATTTCTCC  | 1200 |
| GTGTAGTGTG  | CAACCATGAA  | CATTATATTC | CGTTGAACCT  | ACCAATGCCA | TTTGGAAAAG  | GCAGGATTC   | AAGATACCAA  | 1280 |
| GACCTCCAGC  | TTGACTACTC  | ATTAACAGAT | GAGTTCTGCA  | GAAACCACTT | CTTGGTGGGA  | CTGTTACTGA  | GGGAGGTGGG  | 1360 |
| GACAGCCCTC  | CAGGAGTTCC  | GGGAGGTCCG | TCTGATCGCC  | ATCAGTGTGC | TCAAGAACCT  | GCTGATAAAG  | CATTCTTTTG  | 1440 |
| ATGACAGATA  | TGCTTCAAGG  | AGCCATCAGG | CAAGGATAGC  | CACCTCTAC  | CTGCCCTCTG  | TTGGTCTGCT  | CCCTGGCTCT  | 1520 |
| GTCCAGCGGA  | TCAATGTGAG  | GGATGTGTCA | CCCTTCCCTG  | TGAAACGCGG | CATGACCGTG  | AAGGATGAAT  | CCCTGGCTCT  | 1600 |
| ACCAGCTGTG  | AAATCCGCTGG | TGACGCGCGA | GAAGGGAAGC  | ACCTGTGACA | ACAGCCTGCA  | CAAGGACCTG  | CTGGGCGCCA  | 1680 |
| TCTCCGCGAT  | TGCTTCTCCA  | TATACAACCT | CACTCCAAA   | CATCAACAGT | GTGAGAAATG  | CTGATTCGAG  | AGGATCTCTC  | 1760 |
| ATAAGCACAG  | ATTCCGGTAA  | CAGCCTTCCA | GAAGGGAATA  | GTGAGAAGAG | CAATTCCTTG  | GATAAGCAC   | AACAAAGTAG  | 1840 |
| CACATTGGGA  | AATTCGGTGG  | TTGCTGTGTA | TAAACTTGAC  | CAGTCTGAGA | TTAAGAGCCT  | ACTGATGTGT  | TTCTCTTACA  | 1920 |
| TCTTAAAGAG  | CATGCTGTAT  | GATGCTTTGT | TTACATATTG  | GAACAAGGCT | TCAACATCTG  | AACCTTATGA  | TTTTTTTACA  | 2000 |
| ATATCTGAAG  | TCTGCCCTCA  | CCAGTTCCAG | TACATGGGGA  | AGCGATACAT | AGCCAGGAAC  | CAGGAGGGGT  | TGGGACCCAT  | 2080 |
| AGTTCTATGAT | CGAAAGTCTC  | AGACATTGCC | TGTTTCCCGT  | AACAGAACAG | GAATGATGCA  | TGCCAGATTG  | CATCAGCTGG  | 2160 |
| GCAAGCTGGA  | TAACTCTCTC  | ACTTTTAACC | ACAGCTATGG  | CCACTCGGAC | GCAGATGTTT  | TGCACCACTC  | ATTACTGAA   | 2240 |
| GCCAAAGATT  | CTACTGAGGT  | TTGCCGTGCA | GCTCTGGACA  | CGCTTTCTCT | ATTTACATTG  | GCGTTTAAAG  | ACCAGCTCCT  | 2320 |
| GGCGAACCAT  | GGACATAATC  | CTCTCATGAA | AAAAGTTTTT  | GATGTCTACC | TGTGTTTTCT  | TCAAAAACAT  | CAGTCTGAAA  | 2400 |
| CGGCTTAA    | AAATGCTCTC  | ACTGCCTTAA | GGTCTTAAT   | TTATAAGTTT | CCCTCAACAT  | TCTATGAAGG  | GAGAGCGGAC  | 2480 |
| ATATGTCGCG  | CTCTGCTTAA  | CGAGATCTCT | AAGTGTCTGA  | ACTCCAAGCT | GAGCTCCATC  | AGGACCGAGG  | CCTCCAGCT   | 2560 |
| GCTCTACTTC  | CTGATGAGGA  | ACAACTTTGA | TTACACTGGA  | AAGAAGTCTT | TTGTCCGGAC  | ACATTTCGAA  | GTCTCATAT   | 2640 |
| CTGTCTAGCCA | GCTGATAGCA  | GACGTGTGTG | GCATTGGGGA  | AACCAGATTC | CAGCAGTCCC  | TGTCCATCAT  | CAACAAGTGT  | 2720 |
| GCCAAACAGT  | ACCGGCTTAT  | TAAAGCACCC | AGCTTCTCCT  | CTGATGTGAA | GGACTTAACC  | AAAAGGATAC  | GCACGCTGCT  | 2800 |
| AATGCCACCC  | GCCAGATGTA  | AGGAGCATGA | GAACGACCCA  | GAGATGCTGG | TGGACCTCCA  | GTACAGCCTG  | GCCAAATCCT  | 2880 |
| ATGCCAGTAC  | GCCCGAGCTC  | AGGAAGACGT | GGCTCGACAG  | CATGGCCATG | ATCCATGTCA  | AAAATGGGGA  | TCTCTCAGAG  | 2960 |
| CGCAGATGT   | GCTATGTCCA  | CGTAACAGCC | CTAGTGGCAG  | AATATCTCAC | ACGGAAGGCG  | GTGTTTAGAC  | AAGGATGCAC  | 3040 |
| CGCCTTCAGG  | GTCAATTACC  | CAAACTCGA  | CGAGGAGGCC  | TCCATGATGG | AAGACGTGGG  | GATGCGAGAT  | GTCCATTTC   | 3120 |
| ACGAGGATGT  | GCTGATGGAG  | CTCCTTGAGC | AGTGCGCAGA  | TGGACTCTGG | AAAGCCGAGC  | GCTACGAGCT  | CATGCGCGAC  | 3200 |
| ATCTCAAAAC  | TTATCATCCC  | CATTATATG  | AAGCGGAGGG  | ATTTCTTTGA | AGATGAAGAT  | TGTAATTTGGT | TTCTGAAAATG | 3280 |
| GGAACTCAAA  | CTCACACGCG  | TGTCCGAAAT | TTCTCAGAGA  | CTCCTTAAAC | TGTAATTTGGT | TAAATTTGGT  | TCTGAAAATG  | 3360 |
| TCATTAATGAT | ACAGGATTCT  | GGCAAGGTCA | ACCTTAAGGA  | TCTGGATTCT | AAGTATGCAT  | ACATCCAGGT  | GACTCACTGC  | 3440 |
| ATCTCTTCTT  | TGACGAAAA   | AGAGTTGCAA | GAAGGAAAA   | CAGAGTTTGA | GAGATCCAC   | AACATCCGCT  | GCTTCATGTT  | 3520 |
| TGAGATGCCA  | TTTACGCGA   | CGGGAAGAG  | GCAGGGCGGG  | GTGGAAGAGC | AGTGCAACG   | GCGCACCATC  | CTGACAGCCA  | 3600 |
| TACATGCTTT  | CCCTTATGTG  | AAGAAGCGCA | TCCCTGTCTAT | GTAACGACAC | CACACTGACC  | TGAACCCCAT  | CGAGGTGGCC  | 3680 |
| ATTCAGCAGA  | TGAGTAAGAA  | GGTGGCGGAG | CTCCGCGAGC  | TGTGCTCTTC | GGCCGAGGTG  | GACATGATCA  | AACCTCAGCT  | 3760 |
| CAAACTCCAG  | GGCAGCGTGA  | GTGTTCAAGT | CAATGCTGGC  | CCACTAGCAT | ATGCGCGAGC  | TTTCTTAGAT  | GATACAAACA  | 3840 |
| CAAAAGCGATA | TCTTGCAAT   | AAAGTGAAGC | TGCTTAAGGA  | AGTTTTCAGG | CAATTTGTGG  | AAGCTTGGCG  | TCAAGCCTTA  | 3920 |
| GCGGTAAACG  | AACGCTGAT   | TAAAGAAGAC | CAGCTCGAGT  | ATCAGGAAGA | AATGAAAGCC  | AACACAGGG   | AAATGGCGAA  | 4000 |
| GGAGCTTTCT  | GAAATCATGC  | ATGAGCAGAT | CTGCCCCCTG  | GAGGAGAAGA | CGAGCGTCTT  | ACCGAATTCC  | CTTCACTCT   | 4080 |
| TCAACGCCAT  | CAGTGGGACT  | CCAACAAGCA | CAATGGTTCA  | CGGGATGACC | AGCTCGTCTT  | CGGTGCTGTG  | ATTACATCTC  | 4160 |
| ATGCCCGCTG  | TGTGGGACT   | TGCTTTGTCA | TTTGCAAACT  | CAGGATGCTT | TCCAAAGCCA  | ATCACTGGGG  | AGACCGAGCA  | 4240 |
| CAGGAGGAC   | CAAGGGGAAG  | GGGAGAGAAA | GGAAATAAAG  | AACAACGTTA | TTTCTTAAAC  | GACTTTCTAT  | AGGAGTTGTA  | 4320 |
| AGAAGGTGCA  | CATATTTTTT  | TAAATCTCAC | TGGCAATATT  | CAAAGTTTTT | ATGTGTCTT   | AACAAAGGTG  | TGGTAGACAC  | 4400 |
| TCTTGAGCTG  | GACTTAGATT  | TTATTTCTCC | TTGCAAGTAT  | GTGTTAGAA  | AGATGGCCTA  | CAGAAAAAAA  | AGGTTCTGGG  | 4480 |
| ATCTACATGG  | CAGGAGGGGC  | TGCACTGACA | TTGATGCCCTG | GGGGACCTTT | TGCTCGACT   | CGTGCCGGAA  | ATCTGATCCT  | 4560 |
| AATCAGGGTA  | CAGAATTAC   | TAGTTTGTGC | TAGGAGTATG  | TTGTATGACT | AGGATTTGTG  | CTATTATCTC  | ATTCAACAAC  | 4640 |
| ATAGAGCAAG  | AATAGTGAGC  | TAACTGAGCT | AGCACTCAA   | TTAATCCGCT | ACTGCGCTCA  | AGTCAGAACT  | TTGTCAITAA  | 4720 |
| TCATCGACTC  | CGGAGCGGTC  | ATATATGAT  | TACATTTCTA  | CATTTTTAAT | ACTCACATGG  | GCTTATGCAT  | TAAGTTTAA   | 4800 |
| TGTGATAAAT  | TTGTGCTGGT  | CCAGTATATG | CAATACACTT  | TAATGGTTA  | TTCTGTCTAT  | AAAAATGTGC  | AATATGGAGA  | 4880 |
| TGTATACAAG  | TCITTAAT    |            |             |            |             |             |             | 4898 |



|           |            |            |            |            |            |             |                 |
|-----------|------------|------------|------------|------------|------------|-------------|-----------------|
| 10        | 20         | 30         | 40         | 50         | 60         | 70          | 80              |
| HVMIAPL   | PTILNQLFRV | LTRATQEEVA | VNVTRVIIHV | VAQCHEEGLE | SHLRSYVKYA | YKAEPIVASE  | YKTVHEELTK 80   |
| TILKPSA   | DFLTSNILLR | YSWFFFDVLI | KSMACHLIEN | SKVKLLRNOR | FPASYHHAAE | TVVNMIMPHI  | TOKFGDNFEA 160  |
| ANHSLAV   | FIKRCFTFMD | RGFVFKQINN | YISCFAPGDP | KTLFEYKFEP | LRVVCNHEHY | IPLNLPMPFG  | KGRICRYOOD 240  |
| YSLTDEF   | CRNHFLVGLL | LREVGTAQOE | FREVRLIAIS | VILNLLIKHS | FDDRYASRSH | QARIATLYLF  | LPGLLIENVO 320  |
| VRDVSPF   | PVNAGMTVKD | ESLALFAVNP | LVTPOKGSTL | DNSLHKDLLG | AISGIASPYT | TSTFNINSVR  | NADSRGSLIS 400  |
| IGNSLPER  | NSEKSNSLDK | HQOSSTLGNS | VVRCDKLDQS | EIKSLIMCFL | YILKMSDDA  | LPTYWNKAST  | SELMOPFTIS 480  |
| LNHQPQYM  | GKRYIARNOE | GLGPIVHDRK | SOTLPVSRNR | TGMHARLQQ  | LGLSLSLTF  | NHSYGHSDAD  | VLHOSLLEAN 560  |
| FEVCLTAL  | DTLSLFTLAF | KNQLLADHGH | NPLMKKVFQV | YLCFLQKHQS | ETALKQVFTA | LRLTYKFPFS  | TFYBGRADMC 640  |
| UCYEILKC  | CNSKLSIRT  | EASQLLYFLM | RNNFDYTGKK | SFVRTHLOVI | ISVSQLLADV | VGIGETRPOQ  | SLSIINNCAN 720  |
| RLIKHTSF  | SSDVKDLTKR | IRTVLMATAQ | MKEHENDPEM | LVDLQYSLAK | SYASTPELRK | TWLDSEARH   | VKNGDLSEAA 800  |
| YVHVITALV | AEYLTRUGVF | ROGCTAFRVI | TPNIDEEASN | MEDVGMQDVH | FNEDVLMELL | EQCADGLWKA  | ERYELIADIY 880  |
| IIPIYKRR  | KDFFEDEDGK | EYIYKEPKLT | PLSEISORLL | KLYSDKFGSE | NVKMIQDSGK | VNPKOLDISKY | AYIQVTHVIP 960  |
| DEKELQER  | KTEFERSHNI | RRFMFEMPFT | QTGKROGGVE | EQCKRRTILT | AIHCFFPVKK | RIPVMYQHHT  | DLNPIEVAID 1040 |
| ISKVVAELR | QLCSSAEVDM | IKLQKLGQS  | VSVQVNAGPL | AYARAPLDDT | NTKRYPDNKV | KLLKEVFRQF  | VEACGOALAV 1120 |
| RLIKEDOL  | EYQEEMKANY | REMAKELSEI | MHEQICPLEE | KTSVLPNSLH | IFNAISGTFT | STMVHGTTSS  | SSVV 1194       |
| 10        | 20         | 30         | 40         | 50         | 60         | 70          | 80              |

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FIG. 10F (cont.)

|      | 10          | 20          | 30          | 40          | 50          | 60          | 70         | 80          |
|------|-------------|-------------|-------------|-------------|-------------|-------------|------------|-------------|
| 1    | AATTGTAATA  | CGACTCACTA  | TAGGGCGAAT  | TGGGTACGGG  | GCCCCCCTC   | GAGGTGACG   | GTATCGATAA | GCTTGATATC  |
| 81   | GAATTCGGCA  | CGAGTTTTAC  | ACCATCACCA  | AAACCCAGAA  | TTTTATGATG  | AGATTAAAAAT | AGAGTTGCC  | ACTCAGCTGC  |
| 161  | ATGAAAAGCA  | CCACCTGTTG  | CTCACAATCT  | TCCATGTCAG  | CTGTGACAAC  | TCAAGTAAAG  | GAAGCACGAA | GAAGAGGGAT  |
| 241  | GTCTTTGAAA  | CCCAAGTTGG  | CTACTCCTGG  | TCTCCCTCC   | TGAAAGACGG  | AAGGGTGGTG  | ACAAGCGAGC | AGCACATCCC  |
| 321  | GGTCTCGGCG  | AACCTTCCCT  | CGGGCTATCT  | TGGCTACCAA  | GAGCTTGGGA  | TGGGCAGGCA  | TTATGGTCCG | GAAATTAAAT  |
| 401  | GGGTAGATGG  | AGGCAAGCCA  | CTGCTGAAAA  | TTTCCACTCA  | TCTGTTTCT   | ACAGGGATAC  | TCAGGATCAG | CATTTCATA   |
| 481  | ATTTTTTCCA  | GTACTGTCAG  | AAAACCGAAT  | CTGGAGCCCA  | AGCCTTAGGA  | AACGAACTTG  | TAAAGTACCT | TAAGAGTCTG  |
| 561  | CATGCGATGG  | AAGGCCACGT  | GATGATCGCC  | TCTTGCCCA   | CTATCTTAA   | CCAGCTGTTT  | CGAGTCTCTA | CCAGAGCCAC  |
| 641  | ACAGGAAGAA  | GTCGCGGTTA  | ACGTGACTCG  | GGTCATTATT  | CATGTGGTTG  | CCCAGTGCCA  | TGAGGAAGGA | TTGGAGAGCC  |
| 721  | ACTTGAGGTC  | ATATGTTAAG  | TACGCGTATA  | AGGCTGAGCC  | ATATGTTGCC  | TCTGAATACA  | AGACAGTGCA | TGAAGAACTG  |
| 801  | ACCAAAATCCA | TGACCACGAT  | TCTCAAGCCT  | TCTGCCGATT  | TCCCTCACCAG | CAACAAACTA  | CTGAGGTAAT | CATGGTTTTT  |
| 881  | CTTTGATGTA  | CTGATCAAAT  | CTATGGCTCA  | GCATTTGATA  | GAGCACTCCA  | AAGTTAAGTT  | GCTGGGAAAC | CAGAGATTTT  |
| 961  | CTGCATCCTA  | TCATCATGCA  | GCGGAAACCG  | TTGTAATAT   | GCTGATGCCA  | CACATCACTC  | AGAAGTTTGG | AGATAATCCA  |
| 1041 | GAGGCATCTA  | AGAACGCGAA  | TCATAGCCTT  | GCTGTCTTCA  | TCAAGAGATG  | TTTCACTTTC  | ATGGACAGGG | GCTTTGTCTT  |
| 1121 | CAAGCAGATC  | AACAACCTACA | TTAGCTGTTT  | TGCTCTCTGA  | GACCCAAAGA  | CCCTCTTTGA  | ATACAAGTTT | GAATTTCTCC  |
| 1201 | GTGTAGTGTG  | CAACCATGAA  | CATTATATTC  | CGTTGAACCT  | ACCAATGCCA  | TTTGGAAAAG  | GCAGGATTTA | AAGATACCAA  |
| 1281 | GACCTCCAGC  | TTGACTACTC  | ATTAACAGAT  | GAGTTCTGCA  | GAAACCACTT  | CTTGGTGGGA  | CTGTTACTGA | GGGAGGTGGG  |
| 1361 | GACAGCCCTC  | CAGGAGTTCC  | GGGAGGTCG   | TCTGATCGCC  | CACCTCTTAC  | TCAAGAACCT  | GCTGATAAAG | CATTCTTTTG  |
| 1441 | ATGACAGATA  | TGCTTCAAGG  | AGCCATCAGG  | CAAGGATAGC  | TGAACGCGGG  | CATGACCGTG  | AAGGATGAAT | CCCTGGCTCT  |
| 1521 | GTCCAGCGGA  | TCAATGTGAG  | GGATGTGTCA  | CCCTTCCCTG  | ACCTTGGACA  | ACAGCCTGCA  | CAAGGACCTG | CTGGGCGCCA  |
| 1601 | ACCAGCTGTG  | AATCCGCTGG  | TGACGCGGCA  | GAAGGGAAGC  | CATCAACAGT  | GTGAGAAATG  | CTGATTGAG  | AGGATCTCTC  |
| 1681 | TCCTCCGGCAT | TGCTTCTCCA  | TATACAACCT  | CAACTCCAAA  | GTGAGAAGAG  | CAATTCCCTG  | GATAAGCACC | AACAAGTAG   |
| 1761 | ATAAGCACAG  | ATTCCGGTAA  | CAGCCTTCCA  | GAAAGGAATA  | CAGTCTGAGA  | TTAAGAGCCT  | ACTGATGTGT | TTCTCTACA   |
| 1841 | CACATTGGGA  | AATTCCGTGG  | TTCCGTGTGA  | TAAACTTGAC  | GAACAAGGCT  | TCAACATCTG  | AACATTATGA | TTTTTTTACA  |
| 1921 | TCTTAAAGAG  | CATGCTGAT   | GATGCTTTGT  | TTACATATTG  | AGCGATACAT  | AGCCAGGAAC  | CAGGAGGGGT | TGGGACCCAT  |
| 2001 | ATATCTGAAG  | CTGCGCTGCA  | CCAGTTCCAG  | TACATGGGGA  | AACAGAACAG  | GAATGATGCA  | TGCCAGATTG | CAGCAGCTGG  |
| 2081 | AGTTCAATGAT | CGAAAGTCTC  | AGACATTGCC  | TGTTTTCCGT  | CCACTTGGAC  | GCAGATGTTT  | TGCACCACTG | ATTACTTGAA  |
| 2161 | GCAGCCTGGA  | TAACTCTCTC  | ACTTTTAAAC  | ACAGCTTATG  | CGCTTTCTCT  | ATTTACATTG  | CGGTTTAAAG | ACCAGCTCCT  |
| 2241 | GCCAACTTGG  | CTACTGAGGT  | TTGCCGTGACA | GCTCTGGACA  | GATGCTTACC  | TGTTTCTTCT  | TCAAAAACAT | CAGTCTGAAA  |
| 2321 | GGCCGACCAT  | GGACATAATC  | CTCTCATGAA  | AAAAGTTTTT  | TTATAAGTTT  | CCCTCAACAT  | TCTATGAAG  | GAGAGCGGAC  |
| 2401 | CGGCTTTAAA  | AAATGTCTTC  | ACTGCCTTAA  | GGTCCCTTAA  | ACTCCAAGCT  | GAGCTCCATC  | AGGACGGAGG | CTCCAGCT    |
| 2481 | ATGTGTGCGG  | CTCTGTGTTA  | CGAGATTCTC  | AAGTGTCTGA  | AAGAAGTCTT  | TTGTCCGGAC  | ACATTGCAA  | GTCATCATAT  |
| 2561 | GCTCTACTTC  | CTGATGAGGA  | ACAACCTTGA  | TTCACTGGGA  | AACCAAGTCT  | CAGCAGTCCC  | TGTCATCAT  | CAACAACTGT  |
| 2641 | CTGTGAGCCA  | GCTGATAGCA  | GACGTTGTTG  | GGATTGGGGA  | CTGATGTGAA  | GGACTTAACC  | AAAAGGATAC | GCCAAATCCT  |
| 2721 | GCCAAACAGT  | ACCGGCTTAT  | TAAAGCACAC  | AGCTTCTCCT  | GAGATGCTGG  | TGGACCTCCA  | GTACAGCCTG | TCTCTCAGAG  |
| 2801 | AATGGCCACC  | GCCCGAGCTC  | AGGAGCATGA  | GAACGACCCA  | CATGCGGAC   | ATCCATGTCA  | AAAATGGCGA | AGGATGAC    |
| 2881 | ATGCCAGCAC  | GCCCGAGCTC  | AGGAGACGCT  | GGCTCGACAG  | AATATCTCAC  | ACGGAAGGCG  | GTGTTTAGAC | GTCCATTTC   |
| 2961 | GCAGCAATGT  | GCTATGTCCA  | CGTAACAGCC  | CTAGTGGCAG  | TCCATGATGG  | AAGACGTGGG  | GATGCAAGAT | CATCGCCGAC  |
| 3041 | CGCTCTCAGG  | GCTATGATCC  | CAACATCGA   | CGAGGAGGCC  | TGGACTCTGG  | AAAGCCGAGC  | GCTACGAGCT | ATATTTACAA  |
| 3121 | ACGAGGATGT  | GCTGATGGAG  | CTCCTTGAGC  | AGTGGCAGGA  | ATTTCTTTGA  | AGATGAAGAT  | GGAAAGGAGT | TCTGAAAATG  |
| 3201 | ATCTACAAAC  | TTATCATCCC  | CATTATGAG   | AAGCGGAGGG  | CTCCTTAAAC  | TGTACTCGGA  | TAAATTTGGT | GACTCAAGCT  |
| 3281 | GGAACCCAAA  | CTCACACCGC  | TGTCGGAAT   | TTCTCAGAGA  | CTCTGATTCT  | AAGTATGCAT  | ACATCCAGGT | GCTTCATGTT  |
| 3361 | TCAAAATGAT  | ACAGGATTCT  | GGCAAGGTCA  | ACCCTAAGGA  | CAGAGTTTGA  | GAGATCCCAC  | AACATCCGCC | GCTTCATGTT  |
| 3441 | ATCCCTTCTT  | TTGACGAAAA  | CCGGGAAGAG  | GCAGGGCGGG  | GTGGAAGAGC  | AGTGCAAACG  | GCGCACCATC | CTGACAGCCA  |
| 3521 | TGAGATGCCA  | TTTACGCAGA  | AAGAAGCGCA  | TCCCCTGTCAT | GTACCAGCAC  | CACACTGACC  | TGAACCCCAT | CGAGGTGGCC  |
| 3601 | TACACTGCCT  | CCCTTATGTG  | AAGAAGCGCA  | TCCCCTGTCAT | TGTGCTCCTC  | GGCCGAGGTG  | GACATGATCA | AACTGCAGCT  |
| 3681 | ATTGACGAGA  | TGAGTAAGAA  | GGTGGCGGAG  | CTCCGGCAGC  | CCACTAGCAT  | ATGCGCGAGC  | TTTCTTAGAT | GATACAAACA  |
| 3761 | CAAACTCCAG  | GGCAGCGTGA  | GTGTTCAAGT  | CAATGCTGGC  | AGTTTTTCAGG | CAATTTGTGG  | AAGCTTGGCG | TCAAGCCTTA  |
| 3841 | CAAAGCGATA  | TCCTGACAAAT | AAAGTGAAGC  | TGCTTAAGGA  | ATCAGGAAGA  | AATGAAAGCC  | AACTACAGGG | AAATGGCGAA  |
| 3921 | GCGGTAAACG  | AACGTCTGAT  | TAAAGAAGAC  | CAGCTCGAGT  | GAGGAGAAGA  | CGAGCGTCTT  | ACCGAATTCC | CTTCACATCT  |
| 4001 | GGAGCTTTCT  | GAAATCATGC  | ATGAGCAGAT  | CTGCCCCCTG  | CGGGATGACC  | AGCTCGTCTT  | CGGTGCTGTG | ATTACATCTC  |
| 4081 | TCAACGCCAT  | CAGTGGGACT  | CCAACAAGCA  | CAATGGTTCA  | CAGGATGCTT  | TCCAAAGSCA  | ATCACTGGGG | AGACCGAGCA  |
| 4161 | ATGGCCCGTG  | TGTGGGGACT  | TGCTTTGTCA  | TTTGCAAACT  | AACAACGTTA  | TTTCTTAACA  | GACTTCTAT  | AGGAGTTGTA  |
| 4241 | CAGGGAGGAC  | CAAGGGGAAG  | GGGAGAGAAA  | GGAAATAAAG  | CAAAGTTTTC  | ATTGTGCTCT  | AACAAAGGTG | TGGTAGACAC  |
| 4321 | AGAAGGTGCA  | CATATTTTTT  | TAAATCTCAC  | TGGCAATATT  | GTGTTAGAAT  | AGATGGCCTA  | CAGAAAAAAA | AGGTTCTGGG  |
| 4401 | TCTTGAGCTG  | GACTTAGATT  | TTATTCTTCC  | TTGCAGAGTA  | GGGGACCTTT  | TGCCCTCGACT | CGTGCCGGAA | ATCTGATCGT  |
| 4481 | ATCTACATGG  | CAGGGAGGGC  | TGCACTGACA  | TTGATGCCCTG | TTGTATGACT  | AGGATTTGTG  | CTATTATCTC | ATTCAACAAC  |
| 4561 | AATCAGGGTA  | CAGAACTTAC  | TAGTTTTGTC  | TAGGAGTATG  | TTAATCCGCT  | ACTGGCTTCA  | AGTCAGAACT | TTGTCAATTA  |
| 4641 | ATAGAGCAAG  | AATAGTGAGC  | TAACTGAGCT  | AGACACTCAA  | CATTTTAAAT  | ACTCACATGG  | GCTTATGCAT | TAAGTTTAAAT |
| 4721 | TCATCGACTC  | CGGACCGGTC  | ATATATGTAT  | TACATTTCTA  | TAATGGTTTTA | TTCTTGTCTAT | AAAAATGTGC | AATATGGAGA  |
| 4801 | TGTGATAAAT  | TTGTGCTGGT  | CCAGTATATG  | CAATACACTT  |             |             |            | 4880        |
| 4881 | TGTATACAAG  | TCCTTACT    |             |             |             |             |            | 4898        |

Fig. 106

|      | 10         | 20          | 30          | 40          | 50          | 60          | 70          | 80         |      |
|------|------------|-------------|-------------|-------------|-------------|-------------|-------------|------------|------|
| 1    | MEGHVMI    | PTILNQLFRV  | LTRATQEEVA  | VNVTRVIIHV  | VAQCHEEGLE  | SHLRSYVKYA  | YKAEPYVASE  | YKTVHEELTK | 80   |
| 81   | SMTTILKPSA | DFLTSNKLLR  | YSWFFFDVLI  | KSMAQH LIEN | SKVKLLRNQR  | FPASYHHAEE  | TVVNMLMPHI  | TQKPGDNPEA | 160  |
| 161  | SKNANHSLAV | FIKRCFTFMD  | RGFVFKQINN  | YISCFAPGDP  | KTLFEYKFEF  | LRVVCNHEHY  | IPLNLPMPFG  | KGRIQRYQDL | 240  |
| 241  | QLDYSLTDEF | CRNHFLVGLL  | LREVG TALQE | FREVRLIAIS  | VLKNLLIKHS  | FDDRYASRSH  | QARIATLYLP  | LPGLLIENVQ | 320  |
| 321  | RINVRDVSPF | PVNAGMTVKD  | ESLALPAVNP  | LVTPQKGSTL  | DNSLHKDLG   | AISG IASPYT | TSTPNINSVR  | NADSRGSLIS | 400  |
| 401  | TDSGNSLPER | NSEKSNSLDK  | HQQSSTLGNS  | VVRCDKLDQS  | EIKSLIMCFL  | YILKSMSDDA  | LFTYWNKAST  | SELMDFFTIS | 480  |
| 481  | EVCLHQFOYM | GKRYIARNQE  | GLGPIVHDRK  | SQTLPVSRNR  | TGMMHARLOQ  | LGSLDNSLTF  | NHSYGHSDAD  | VLHQSLLEAN | 560  |
| 561  | IATEVCLTAL | DTLSLFTLAF  | KNQLLADHGH  | NPLMKKVFDV  | YLCFLOKHQS  | ETALKNVFTA  | LRSLIYKFPS  | TFYEGRADMC | 640  |
| 641  | AALCYEILKC | CNSKLSSIRT  | EASQLLYFLM  | RNNFDYTGKK  | SFVRTHLQVI  | ISVSQLIADV  | VGIGETRFOQ  | SLSIINNCAN | 720  |
| 721  | SDRLIKHTSF | SSDVKDLTKR  | IRTVLMTAQ   | MKEHENDPEM  | LVDLQYSLAK  | SYASTPELRK  | TWLD SMARIH | VKNGDLSEAA | 800  |
| 801  | MCYVHVITLV | AEYLTRKGVF  | ROGCTAFRVI  | TPNIDEEASM  | MEDVGMQDVH  | FNEDVLMELL  | EQCADGLWKA  | ERYELIADIY | 880  |
| 881  | KLIPIIYEKR | RDFFEDEDGK  | EYIYKEPKLT  | PLSEISQRLI  | KLYSDKFGSE  | NVKMIQDSGK  | VNPKDLD SKY | AYIQVTHVIP | 960  |
| 961  | FFDEKELQER | KTEFERSHNI  | RRFMFEMPFT  | QTGKRQGGVE  | EQCKRRRTILT | AIHCFFPYVK  | RIPVMYQHHT  | DLNPIEVAID | 1040 |
| 1041 | EMSKKVAELR | QLCSSAEVDM  | IKLQKLQGS   | VSVQVNAGPL  | AYARAFLDDT  | NTKRYPDNKV  | KLLKEVFRQF  | VEACGQALAV | 1120 |
| 1121 | NERLIKEDQL | EYQEE MKANY | REMAKELSEI  | MHEQICPLEE  | KTSVLPNSLH  | IFNAISGTPT  | STMVHGMTSS  | SSVV       | 1194 |

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FIG. 10G (cont.)

|      | 10          | 20          | 30          | 40          | 50          | 60          | 70          | 80         |
|------|-------------|-------------|-------------|-------------|-------------|-------------|-------------|------------|
| 1    | AATTGTAATA  | CGACTCACTA  | TAGGGCGAAT  | TGGGTACCGG  | GCCCCCCTC   | GAGGTGACG   | GTATCGATAA  | GCTTGATATC |
| 81   | GAATTCGGCA  | CGAGTTTAC   | ACCATCACCA  | AAACCCAGAA  | TTTTATGATG  | AGATTAAAT   | AGAGTTGCC   | ACTCAGCTGC |
| 161  | ATGAAAAGCA  | CCACCTGTTG  | CTCACATTCT  | TCCATTGTCAG | CTGTGACAAC  | TCAAGTAAAG  | GAAGCACGAA  | GAAGAGGGAT |
| 241  | GTCGTTGAAA  | CCCAAGTTGG  | CTACTCCTGG  | CTTCCCTCC   | TGAAAGACGG  | AAGGGTGGTG  | ACAAGCGAGC  | AGCACATCCC |
| 321  | GGTCTCGGCG  | AACCTTCCTT  | CGGGCTATCT  | TGGCTACCAA  | GAGCTTGGGA  | TGGGCAGGCA  | TTATGGTCCG  | GAAATTAAAT |
| 401  | GGGTAGATGG  | AGGCAAGCCA  | CTGCTGAAAA  | TTTCCACTCA  | TCTGTTTTCT  | ACAGGGATAC  | TCAGGATCAG  | CATTACATA  |
| 481  | ATTTTTTCCA  | GTACTGTGAG  | AAAACCGAAT  | CTGGAGCCCA  | AGCCTTAGGA  | AACGAACTTG  | TAAAGTACCT  | TAAGAGTCTG |
| 561  | CATGCGATGG  | AAGGCCACGT  | GATGATCGCC  | TTCTTGCCCA  | CTATCCTAAA  | CCAGCTGTTT  | CGAGTCCCTCA | CCAGAGCCAC |
| 641  | ACAGGAAGAA  | GTCGCGGTTA  | ACGTGACTCG  | GGTCATTATT  | CATGTGGTTG  | CCCAGTGCCA  | TGAGGAAGGA  | TTGGAGAGCC |
| 721  | ACTTGAGGTC  | ATATGTTAAG  | TACCGGTATA  | AGGCTGAGCC  | ATATGTTGCC  | TCTGAATACA  | AGACAGTGCA  | TGAAGAACTG |
| 801  | ACCAAATCCA  | TGACCACGAT  | TCTCAAGCCT  | TCTGCCGATT  | TCCTCACCAG  | CAACAACTA   | CTGAGGTAAT  | CATGTTTTTT |
| 881  | CTTTGATGTA  | CTGATCAAAT  | CTATGGCTCA  | GCATTTGATA  | GAGAATCCA   | AAGTTAAGTT  | GCTGCGAAAC  | CAGAGATTTC |
| 961  | CTGCATCCTA  | TCTATCATGCA | GCGGAAACCG  | TGTAAATAT   | GCTGATGACA  | CACATCACTC  | AGAAGTTTGG  | AGATAATCCA |
| 1041 | GAGGCATCTA  | AGAACCGGAA  | TCTATAGCCTT | GCTGTCTTCA  | TCAAGAGATG  | TTTCACCTTC  | ATGGACAGGG  | GCTTTGCTTT |
| 1121 | CAAGCAGATC  | AACAACTACA  | TTAGCTGTTT  | TGCTCCTGGA  | GACCCAAAGA  | CCCTCTTGA   | ATACAAAGTT  | GAATTTCTCC |
| 1201 | GTGTAGTGTG  | CAACCATGAA  | CATTATATTC  | CGTTGAACCT  | ACCAATGCCA  | TTTGGAAGG   | GCAGGATTCA  | AAGATACCAA |
| 1281 | GACCTCCAGC  | TTGACTACTC  | ATTAACAGAT  | GAGTCTGCA   | GAACCACTT   | CTTGGTGGGA  | CTGTTACTGA  | GGGAGGTGGG |
| 1361 | GACAGCCCTC  | CAGGAGTTCC  | GGGAGGTCCG  | TCTGATCGCC  | ATCAGTGTGC  | TCAAGAACCT  | GCTGATAAAG  | CAATCTTTTG |
| 1441 | ATGACAGATA  | TGCTTCAAGG  | AGCCATCAGG  | CAAGGATAGC  | CACCTCTAC   | CTGCCCTGT   | TTGGTCTGCT  | GATTGAAAC  |
| 1521 | TCCAGCGGA   | TCAATGTGAG  | GGATGTGCA   | CCCTTCCCTG  | TGAACGCGGG  | CATGACCGTG  | AAGGATGAAT  | CCCTGGCTCT |
| 1601 | ACCAGCTGTG  | AATCCGCTGG  | TGACGCCGCA  | GAAGGGAAGC  | ACCTCTGACA  | ACAGCTTGCA  | CAAGGACCTG  | CTGGGCGCCA |
| 1681 | TCCTCCGGAT  | TGCTTCTCCA  | TATACAACT   | CAACTCCAAA  | CATCAACAGT  | GTGAGAAATG  | CTGATTTCAG  | AGGATCTCTC |
| 1761 | ATAAGCACAG  | ATTCCGGGTA  | CAGCCTTCCA  | GAAGGAATA   | GTGAGAAAG   | CAATTCCCTG  | GATAAGCACC  | AACAAAGTAG |
| 1841 | CACATTGGGA  | AATTCCGTGG  | TTGCTGTGAT  | TAAACTTGAC  | CAGTCTGAGA  | TTAAGAGCCT  | ACTGATGTGT  | TTCTCTTACA |
| 1921 | TCTTAAAGAG  | CATGCTGTAT  | GATGCTTTGT  | TTACATATTG  | GAACAAGGCT  | TCAACATCTG  | AACATTATGGA | TTTCTTACA  |
| 2001 | ATATCTGAAG  | TCTGCCCTGCA | CCAGTTCAG   | TACATGGGGA  | AGCGATACAT  | AGCCAGGAAC  | CAGGAGGGGT  | TGGGACCCAT |
| 2081 | AGTTCATGAT  | CGAAAGTCTC  | AGACATTGCC  | TGTTTCCCGT  | AACAGAACAG  | GAATGATGCA  | TGCCAGATTG  | CAGCAGCTGG |
| 2161 | GCAGCCTGGA  | TAACTCTCTC  | ACTTTTAAAC  | ACAGCTATGG  | CCACTCGGAC  | GCAGATGTTT  | TGCACCAGT   | ATTACTTGAA |
| 2241 | GCCAAACATG  | CTACTGAGGT  | TTGCCGTGACA | GCTCTGAGCA  | CGCTTTCTCT  | ATTTCATATTG | GCGTTTAAAG  | ACCAGCTCCT |
| 2321 | GGCCGACCAT  | GGACATAATC  | CTCTCATGAA  | AAAAGTTTTT  | GATGTCTACC  | TGTTGTTTTCT | TCAAAAACAT  | CAGTCTGAAA |
| 2401 | CGGCTTTAAA  | AAATGTCTTC  | ACTGCCITTA  | GGTCTTAAT   | TTATAAGTTT  | CCCTCAACAT  | TCTATGAAGG  | GAGAGCGGAC |
| 2481 | ATGTGTGCGG  | CTCTGTGTTA  | CGAGATTCTC  | AAGTGTCTGA  | ACTCCAAGCT  | GAGCTCCATC  | AGGACGGAGG  | CCTCCAGCT  |
| 2561 | GCTCTACTTC  | CTGATGAGGA  | ACAACCTTGA  | TTACACTGGA  | AAGAAGTCTT  | TTGTCCGGAC  | ACATTGTCAA  | GTCTCATAT  |
| 2641 | CTGTGAGCCA  | GCTGTAGCA   | GACGTTGTTG  | GCATTGGGGA  | AACCAGATTG  | CAGCAGTCCC  | TGTCCATCAT  | CAACAACTGT |
| 2721 | GCCAAACAGT  | ACCGGCTTAT  | TAAGCACACC  | AGCTTCTCCT  | CTGATGTGAA  | GGACTTAACC  | AAAAGGATAC  | GCACGGTGCT |
| 2801 | AATGGCCACC  | CGCCAGATGA  | AGGAGCATGA  | GAACGACCTC  | GAGATGCTGG  | TGGACCTCCA  | GTACAGCCTG  | GCCAAATCCT |
| 2881 | ATGCCAGCAC  | GCCCGAGCTC  | AGGAAGACGT  | GGCTCGACAG  | CATGCCACAG  | ATCCATGTCA  | AAAATGGCGA  | TCTCTCAGAG |
| 2961 | GCAGCAATGT  | GCTATGTCCA  | CGTAACAGCC  | CTAGTGGCAG  | AATATCTCAC  | ACGGAAGGCG  | GTGTTTAGAC  | AAGGATGCAC |
| 3041 | CGCCTTCAGG  | GTCATTACCC  | CAAACATCGA  | CGAGGAGGCC  | TCCATGATGG  | AAGACGTGGG  | GATGCGAGAT  | GTCCATTTC  |
| 3121 | ACGAGGATGT  | GCTGATGGAG  | CTCCTTGAGC  | AGTGCGCAGA  | TGGACTCTGG  | AAAGCCGAGC  | GCTACGAGCT  | CACTGCCGAC |
| 3201 | ATCTACAAAC  | TTATCATCCC  | CATTATGAG   | AAGCGGAGGG  | ATTTCTTTGA  | AGATGAAGAT  | GGAAAGGAGT  | ATATTTACAA |
| 3281 | GGAAACCCAAA | CTCACACCCG  | TGTCGGAAAT  | TTCTCAGAGA  | CTCCTTAAAC  | TGTACTCGGA  | TAAATTTGGT  | TCTGAAAATG |
| 3361 | TCAAAATGAT  | ACAGGATTCT  | GGCAAGGTCA  | ACCCTAAGGA  | TCTGGATTCT  | AAGTATGCAT  | ACATCCAGGT  | GACTCACGTC |
| 3441 | ATCCCTTTCT  | TTGACGAAAA  | AGAGTTGCAA  | GAAGGAAAAA  | CAGAGTTTGA  | GAGATCCAC   | AACATCCGCC  | GCTTCATGTT |
| 3521 | TGAGATGCCA  | TTTACGCAGA  | CCGGGAAGAG  | GCAGGGGGGG  | GTGGAAGAGC  | AGTGCAAAAC  | GCGCACCATC  | CTGACAGCCA |
| 3601 | TACACTGCTT  | CCCTTATGTG  | AAGAAGCGCA  | TCCCTGTCTAT | GTACCAGCAC  | CACACTGACC  | TGAACCCCAT  | CGAGGTGGCC |
| 3681 | ATTGACGAGA  | TGAGTAAGAA  | GGTGGCGGAG  | CTCCGCGAGC  | TGTGCTCCTC  | GGCCGAGGTG  | GACATGATCA  | AACTGCAGCT |
| 3761 | CAAACTCCAG  | GGCAGCGTGA  | GTGTTACAGT  | CAATGCTGGC  | CCACTAGCAT  | ATGCCGAGC   | TTTCTTAGAT  | GATACAAACA |
| 3841 | CAAAGCGATA  | TCCTGACAAAT | AAAGTGAAGC  | TGCTTAAAGGA | AGTTTTTCAGG | CAATTGTGG   | AAGCTTGGCG  | TCAAGCCTTA |
| 3921 | GCGGTAAACG  | AACGTCTGAT  | TAAAGAGAGC  | CAGCTCGAGT  | ATCAGGAAGA  | AATGAAAGCC  | AACTACAGGG  | AAATGGCGAA |
| 4001 | GGAGCTTTCT  | GAAATCATGC  | ATGAGCAGAT  | CTGCCCCCTG  | GAGGAGAAGA  | CGAGCGTCTT  | ACCGAATTCC  | CTTCACATCT |
| 4081 | TCAACGCCAT  | CAGTGGGACT  | CCAACAGCA   | CAATGGTTCA  | CGGGATGACC  | AGCTCGTCTT  | CGGTGCTGTC  | ATTACATCTC |
| 4161 | ATGGCCCGTG  | TGTGGGGACT  | TGCTTTGTCA  | TTTGCAAACCT | CAGGATGCTT  | TCCAAAGCCA  | ATCACTGGGG  | AGACCGAGCA |
| 4241 | CAGGGAGGAC  | CAAGGGGAAG  | GGGAGAGAAA  | GGAAATAAAG  | AACAACGTTA  | TTTCTTAAAC  | GACTTCTAT   | AGGAGTTGTA |
| 4321 | AGAAAGTGCA  | CATATTTTCT  | TAAATCTCAC  | TGGCAATATT  | CAAAGTTTTC  | ATTGTGCTCT  | AACAAAGGTTG | TGGTAGACAC |
| 4401 | TCTTGAGCTG  | GACTTAGATT  | TTATTCTTCC  | TTGCAGAGTA  | GTGTTAGAAT  | AGATGGCCTA  | CAGAAAAAAA  | AGGTTCTGGG |
| 4481 | ATCTACATGG  | CAGGGAGGGC  | TGCACTGACA  | TTGATGCCCTG | GGGGACCTTT  | TGCCCTGACT  | CGTGCCGGAA  | ATCTGATCGT |
| 4561 | AATCAGGGTA  | CAGAACCTTAC | TAGTTTGTGC  | TAGGAGTATG  | TTGTATGACT  | AGGATTTGTG  | CTATTATCTC  | ATTCAACAAC |
| 4641 | ATAGAGCAAG  | AATAGTGAGC  | TAACTGAGCT  | AGACACTCAA  | TTAATCCGCT  | ACTGGCTTCA  | AGTCAGAACT  | TTGTCAATTA |
| 4721 | TCATCGACTC  | CGGAGCGGTC  | ATATATGTAT  | TACATTTCTA  | CATTTTTAAT  | ACTCACATGG  | GCTTATGCAT  | TAAGTTAAAT |
| 4801 | TGTGATAAAT  | TTGTGCTGGT  | CCAGTATATG  | CAATACACTT  | TAATGGTTTA  | TTCTGTGCAT  | AAAAATGTGC  | AATATGGAGA |
| 4881 | TGTATACAG   | TCTTTACT    |             |             |             |             |             | 4898       |
|      | 10          | 20          | 30          | 40          | 50          | 60          | 70          | 80         |

Flg. 10H



Exon 1A (-182 to -102)

GCAGGGGAAAAACCTGGCCCATGATTCACTTACTTCCCACCGGATCTCTCCCATGACACGTGAGGATTA  
TTACAATTTAA -102

Exon 1B (-219 to -102)

TTATCCCTTTACTACTTGCAGAGTGAGTTCGGTAGATGGGAGTGGAGAAGAGAACCTTAGAATCATTGTTTAGTCTTCAT  
CTTTCACAGCTCAGGCTGAAGGCCTTTCCTTGCTGAGA -102

Exon 1C (-143 to -102)

GCGGCAGAGCGTGTCTGAGGTGGTGC GCGGCTCCGTGCTCCT -102

Exon2 and the rest of human CLASP2 cDNA

-101 -79  
GGCAAAGCCAAAGCTAATTGAGC

-78 -1  
AAGCTAATTGAGCCACTCGACTATGAAAATGTCATCGTCCAGAAGAAGACTCAGATCCTGAACGACTGTTTACGGGAG

1/1 31/11  
ATG CTG CTC TTC CCT TAC GAT GAC TTT CAG ACG GCC ATC CTG AGA CGA CAG GGT CGA TAC  
Met leu leu phe pro tyr asp asp phe gln thr ala ile leu arg arg gln gly arg tyr

61/21 91/31  
ATA TGC TCA ACA GTG CCT GCG AAG GCG GAA GAG GAA GCA CAG AGC TTG TTT GTT ACA GAG  
ile cys ser thr val pro ala lys ala glu glu glu ala gln ser leu phe val thr glu

121/41 151/51  
TGC ATC AAA ACC TAT AAC TCT GAC TGG CAT CTT GTG AAC TAT AAA TAT GAA GAT TAC TCA  
cys ile lys thr tyr asn ser asp trp his leu val asn tyr lys tyr glu asp tyr ser

181/61 211/71  
GGA GAG TTT CGA CAG CTT CCG AAC AAA GTG GTC AAG TTG GAT AAA CTT CCA GTT CAT GTC  
gly glu phe arg gln leu pro asn lys val val lys leu asp lys leu pro val his val

241/81 271/91  
TAT GAA GTT GAC GAG GAG GTC GAC AAA GAT GAG GAT GCT GCC TCC CTT GGT TCC CAG AAG  
tyr glu val asp glu glu val asp lys asp glu asp ala ala ser leu gly ser gln lys

301/101 331/111  
GGT GGG ATC ACC AAG CAT GGC TGG CTG TAC AAA GGC AAC ATG AAC AGT GCC ATC AGC GTG  
gly gly ile thr lys his gly trp leu tyr lys gly asn met asn ser ala ile ser val

361/121 391/131  
ACC ATG AGG TCA TTT AAG AGA CGA TTT TTC CAC CTG ATT CAA CTT GGC GAT GGA TCC TAT  
thr met arg ser phe lys arg arg phe phe his leu ile gln leu gly asp gly ser tyr

421/141 451/151  
AAT TTG AAT TTT TAT AAA GAT GAA AAG ATC TCC AAA GAA CCA AAA GGA TCA ATA TTT CTG  
asn leu asn phe tyr lys asp glu lys ile ser lys glu pro lys gly ser ile phe leu

481/161 511/171  
GAT TCC TGT ATG GGT GTC GTT CAG AAC AAC AAA GTC AGG CGT TTT GCT TTT GAG CTC AAG  
asp ser cys met gly val val gln asn asn lys val arg arg phe ala phe glu leu lys

541/181 571/191  
ATG CAG GAC AAA AGT AGT TAT CTC TTG GCA GCA GAC AGT GAA GTG GAA ATG GAA GAA TGG  
met gln asp lys ser ser tyr leu leu ala ala asp ser glu val glu met glu glu trp

601/201 631/211  
ATC ACA ATT CTA AAT AAG ATC CTC CAG CTC AAC TTT GAA GCT GCA ATG CAA GAA AAG CGA  
ile thr ile leu asn lys ile leu gln leu asn phe glu ala ala met gln glu lys arg

661/221 691/231  
AAT GGC GAC TCT CAC GAA GAT GAT GAA CAA AGC AAA TTG GAA GGT TCT GGT TCC GGT TTA  
asn gly asp ser his glu asp asp glu gln ser lys leu glu gly ser gly ser gly leu

721/241 751/251  
GAT AGC TAC CTG CCG GAA CTT GCC AAG AGT GCA AGA GAA GCA GAA ATC AAA CTA AAA AGT  
asp ser tyr leu pro glu leu ala lys ser ala arg glu ala glu ile lys leu lys ser

781/261 811/271  
GAA AGC AGA GTC AAA CTT TTT TAT TTG GAC CCA GAT GCC CAG AAG CTT GAC TTC TCA TCA  
glu ser arg val lys leu phe tyr leu asp pro asp ala gln lys leu asp phe ser ser

841/281 871/291  
GCT GAG CCA GAA GTG AAG TCA TTT GAA GAG AAG TTT GGA AAA AGG ATC CTT GTC AAG TGC  
ala glu pro glu val lys ser phe glu glu lys phe gly lys arg ile leu val lys cys

901/301 931/311  
AAT GAT TTA TCT TTC AAT TTG CAA TGC TGT GTT GCC GAA AAT GAA GAA GGA CCC ACT ACA  
asn asp leu ser phe asn leu gln cys cys val ala glu asn glu glu gly pro thr thr

961/321 991/331  
AAT GTT GAA CCT TTC TTT GTT ACT CTA TCC CTG TTT GAC ATA AAA TAC AAC CGG AAG ATT  
asn val glu pro phe phe val thr leu ser leu phe asp ile lys tyr asn arg lys ile

1021/341 1051/351  
TCT GCC GAT TTC CAC GTA GAC CTG AAC CAT TTC TCA GTG AGG CAA ATG CTC GCC ACC ACG  
ser ala asp phe his val asp leu asn his phe ser val arg gln met leu ala thr thr

1081/361 1111/371  
TCC CCG GCG CTG ATG AAT GGC AGT GGG CAG AGC CCA TCT GTC CTC AAG GGC ATC CTT CAT  
ser pro ala leu met asn gly ser gly gln ser pro ser val leu lys gly ile leu his

1141/381 1171/391  
GAA GCC GCC ATG CAG TAT CCG AAG CAG GGA ATA TTT TCA GTC ACT TGT CCT CAT CCA GAT  
glu ala ala met gln tyr pro lys gln gly ile phe ser val thr cys pro his pro asp

1201/401 1231/411  
ATA TTT CTT GTG GCC AGA ATT GAA AAA GTC CTT CAG GGG AGC ATC ACA CAT TGC GCT GAG  
ile phe leu val ala arg ile glu lys val leu gln gly ser ile thr his cys ala glu

1261/421 1291/431  
CCA TAT ATG AAA AGT TCA GAC TCT TCT AAG GTG GCC CAG AAG GTG CTG AAG AAT GCC AAG  
pro tyr met lys ser ser asp ser ser lys val ala gln lys val leu lys asn ala lys

1321/441 1351/451  
CAG GCA TGC CAA AGA CTA GGA CAG TAT AGA ATG CCA TTT GCT TGG GCA GCA AGG ACA TTG  
gln ala cys gln arg leu gly gln tyr arg met pro phe ala trp ala ala arg thr leu

|                                                                                 |          |
|---------------------------------------------------------------------------------|----------|
| 1381/461                                                                        | 1411/471 |
| TTT AAG GAT GCA TCT GGA AAT CTT GAC AAA AAT GCC AGA TTT TCT GCC ATC TAC AGG CAA |          |
| phe lys asp ala ser gly asn leu asp lys asn ala arg phe ser ala ile tyr arg gln |          |
| 1441/481                                                                        | 1471/491 |
| GAC AGC AAT AAG CTA TCC AAT GAT GAC ATG CTC AAG TTA CTT GCA GAC TTT CGG AAA CCT |          |
| asp ser asn lys leu ser asn asp asp met leu lys leu leu ala asp phe arg lys pro |          |
| 1501/501                                                                        | 1531/511 |
| GAG AAG ATG GCT AAG CTC CCA GTG ATT TTA GGC AAT CTA GAC ATT ACA ATT GAT AAT GTT |          |
| glu lys met ala lys leu pro val ile leu gly asn leu asp ile thr ile asp asn val |          |
| 1561/521                                                                        | 1591/531 |
| TCC TCA GAC TTC CCT AAT TAT GTT AAT TCA TCA TAC ATT CCC ACA AAA CAA TTT GAA ACC |          |
| ser ser asp phe pro asn tyr val asn ser ser tyr ile pro thr lys gln phe glu thr |          |
| 1621/541                                                                        | 1651/551 |
| TGC AGT AAA ACT CCC ATC ACG TTT GAA GTG GAG GAA TTT GTG CCC TGC ATA CCA AAA CAC |          |
| cys ser lys thr pro ile thr phe glu val glu glu phe val pro cys ile pro lys his |          |
| 1681/561                                                                        | 1711/571 |
| ACT CAG CCT TAC ACC ATC TAC ACC AAT CAC CTT TAC GTT TAT CCT AAG TAC TTG AAA TAC |          |
| thr gln pro tyr thr ile tyr thr asn his leu tyr val tyr pro lys tyr leu lys tyr |          |
| 1741/581                                                                        | 1771/591 |
| GAC AGT CAG AAG TCT TTT GCC AAG GCT AGA AAT ATT GCG ATT TGC ATT GAA TTC AAA GAT |          |
| asp ser gln lys ser phe ala lys ala arg asn ile ala ile cys ile glu phe lys asp |          |
| 1801/601                                                                        | 1831/611 |
| TCA GAT GAG GAA GAC TCT CAG CCC CTT AAG TGC ATT TAT GGC AGA CCT GGT GGG CCA GTT |          |
| ser asp glu glu asp ser gln pro leu lys cys ile tyr gly arg pro gly gly pro val |          |
| 1861/621                                                                        | 1891/631 |
| TTC ACA AGA AGC GCC TTT GCT GCA GTT TTA CAC CAT CAC CAA AAC CCA GAA TTT TAT GAT |          |
| phe thr arg ser ala phe ala ala val leu his his his gln asn pro glu phe tyr asp |          |
| 1921/641                                                                        | 1951/651 |
| GAG ATT AAA ATA GAG TTG CCC ACT CAG CTG CAT GAA AAG CAC CAC CTG TTG CTC ACA TTC |          |
| glu ile lys ile glu leu pro thr gln leu his glu lys his his leu leu leu thr phe |          |
| 1981/661                                                                        | 2011/671 |
| TTC CAT GTC AGC TGT GAC AAC TCA AGT AAA GGA AGC ACG AAG AAG AGG GAT GTC GTT GAA |          |
| phe his val ser cys asp asn ser ser lys gly ser thr lys lys arg asp val val glu |          |
| 2041/681                                                                        | 2071/691 |
| ACC CAA GTT GGC TAC TCC TGG CTT CCC CTC CTG AAA GAC GGA AGG GTG GTG ACA AGC GAG |          |
| thr gln val gly tyr ser trp leu pro leu leu lys asp gly arg val val thr ser glu |          |
| 2101/701                                                                        | 2131/711 |
| CAG CAC ATC CCG GTC TCG GCG TAC CTT CCT TCG GGC CAT CTT GGC TAC CAA GAG CTT GGG |          |
| glu his ile pro val ser ala tyr leu pro ser gly his leu gly tyr gln glu leu gly |          |
| 2161/721                                                                        | 2191/731 |
| ATG GGC AGG CAT TAT GGT CCG GAA ATT AAA TGG GTA GAT GGA GGC AAG CCA CTG CTG AAA |          |
| met gly arg his tyr gly pro glu ile lys trp val asp gly gly lys pro leu leu lys |          |





3061/1021  
 CAA AGA TAC CAA GAC CTC CAG CTT GAC TAC TCA TTA ACA GAT GAG TTC TGC AGA AAC CAC  
 gln arg tyr gln asp leu gln leu asp tyr ser leu thr asp glu phe cys arg asn his

3121/1041  
 TTC TTG GTG GGA CTG TTA CTG AGG GAG GTG GGG ACA GCC CTC CAG GAG TTC CGG GAG GTC  
 phe leu val gly leu leu leu arg glu val gly thr ala leu gln glu phe arg glu val

3181/1061  
 CGT CTG ATC GCC ATC AGT GTG CTC AAG AAC CTG CTG ATA AAG CAT TCT TTT GAT GAC AGA  
 arg leu ile ala ile ser val leu lys asn leu leu ile lys his ser phe asp asp arg

3241/1081  
 TAT GCT TCA AGG AGC CAT CAG GCA AGG ATA GCC ACC CTC TAC CTG CCT CTG TTT GGT CTG  
 tyr ala ser arg ser his gln ala arg ile ala thr leu tyr leu pro leu phe gly leu

3301/1101  
 CTG ATT GAA AAC GTC CAG CGG ATC AAT GTG AGG GAT GTG TCA CCC TTC CCT GTG AAC GCG  
 leu ile glu asn val gln arg ile asn val arg asp val ser pro phe pro val asn ala

3361/1121  
 GGC ATG ACC GTG AAG GAT GAA TCC CTG GCT CTA CCA GCT GTG AAT CCG CTG GTG ACG CCG  
 gly met thr val lys asp glu ser leu ala leu pro ala val asn pro leu val thr pro

3421/1141  
 CAG AAG GGA AGC ACC CTG GAC AAC AGC CTG CAC AAG GAC CTG CTG GGC GCC ATC TCC GGC  
 gln lys gly ser thr leu asp asn ser leu his lys asp leu leu gly ala ile ser gly

3481/1161  
 ATT GCT TCT CCA TAT ACA ACC TCA ACT CCA AAC ATC AAC AGT GTG AGA AAT GCT GAT TCG  
 ile ala ser pro tyr thr thr ser thr pro asn ile asn ser val arg asn ala asp ser

3541/1181  
 AGA GGA TCT CTC ATA AGC ACA GAT TCG GGT AAC AGC CTT CCA GAA AGG AAT AGT GAG AAG  
 arg gly ser leu ile ser thr asp ser gly asn ser leu pro glu arg asn ser glu lys

3601/1201  
 AGC AAT TCC CTG GAT AAG CAC CAA CAA AGT AGC ACA TTG GGA AAT TCC GTG GTT CGC TGT  
 ser asn ser leu asp lys his gln gln ser ser thr leu gly asn ser val val arg cys

3661/1221  
 GAT AAA CTT GAC CAG TCT GAG ATT AAG AGC CTA CTG ATG TGT TTC CTC TAC ATC TTA AAG  
 asp lys leu asp gln ser glu ile lys ser leu leu met cys phe leu tyr ile leu lys

3721/1241  
 AGC ATG TCT GAT GAT GCT TTG TTT ACA TAT TGG AAC AAG GCT TCA ACA TCT GAA CTT ATG  
 ser met ser asp asp ala leu phe thr tyr trp asn lys ala ser thr ser glu leu met

3781/1261  
 GAT TTT TTT ACA ATA TCT GAA GTC TGC CTG CAC CAG TTC CAG TAC ATG GGG AAG CGA TAC  
 asp phe phe thr ile ser glu val cys leu his gln phe gln tyr met gly lys arg tyr

3841/1281  
 ATA GCC AGG AAC CAG GAG GGG TTG GGA CCC ATA GTT CAT GAT CGA AAG TCT CAG ACA TTG  
 ile ala arg asn gln glu gly leu gly pro ile val his asp arg lys ser gln thr leu

3091/1031  
 TCA TTA ACA GAT GAG TTC TGC AGA AAC CAC  
 gln arg tyr gln asp leu gln leu asp tyr ser leu thr asp glu phe cys arg asn his

3151/1051  
 GGG ACA GCC CTC CAG GAG TTC CGG GAG GTC  
 phe leu val gly leu leu leu arg glu val gly thr ala leu gln glu phe arg glu val

3211/1071  
 CTG CTG ATA AAG CAT TCT TTT GAT GAC AGA  
 arg leu ile ala ile ser val leu lys asn leu leu ile lys his ser phe asp asp arg

3271/1091  
 GCC ACC CTC TAC CTG CCT CTG TTT GGT CTG  
 tyr ala ser arg ser his gln ala arg ile ala thr leu tyr leu pro leu phe gly leu

3331/1111  
 AGG GAT GTG TCA CCC TTC CCT GTG AAC GCG  
 leu ile glu asn val gln arg ile asn val arg asp val ser pro phe pro val asn ala

3391/1131  
 CTA CCA GCT GTG AAT CCG CTG GTG ACG CCG  
 gly met thr val lys asp glu ser leu ala leu pro ala val asn pro leu val thr pro

3451/1151  
 CAC AAG GAC CTG CTG GGC GCC ATC TCC GGC  
 gln lys gly ser thr leu asp asn ser leu his lys asp leu leu gly ala ile ser gly

3511/1171  
 AAC ATC AAC AGT GTG AGA AAT GCT GAT TCG  
 ile ala ser pro tyr thr thr ser thr pro asn ile asn ser val arg asn ala asp ser

3571/1191  
 AAC AGC CTT CCA GAA AGG AAT AGT GAG AAG  
 arg gly ser leu ile ser thr asp ser gly asn ser leu pro glu arg asn ser glu lys

3631/1211  
 AGC ACA TTG GGA AAT TCC GTG GTT CGC TGT  
 ser thr leu gly asn ser val val arg cys

3691/1231  
 CTA CTG ATG TGT TTC CTC TAC ATC TTA AAG  
 asp lys leu asp gln ser glu ile lys ser leu leu met cys phe leu tyr ile leu lys

3751/1251  
 TGG AAC AAG GCT TCA ACA TCT GAA CTT ATG  
 ser met ser asp asp ala leu phe thr tyr trp asn lys ala ser thr ser glu leu met

3811/1271  
 CAC CAG TTC CAG TAC ATG GGG AAG CGA TAC  
 asp phe phe thr ile ser glu val cys leu his gln phe gln tyr met gly lys arg tyr

3871/1291  
 ATA GTT CAT GAT CGA AAG TCT CAG ACA TTG  
 ile ala arg asn gln glu gly leu gly pro ile val his asp arg lys ser gln thr leu

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401300

|                                                                                                 |                                                                                                 |
|-------------------------------------------------------------------------------------------------|-------------------------------------------------------------------------------------------------|
| 3901/1301<br>CCT GTT TCC CGT AAC AGA ACA GGA ATG ATG<br>pro val ser arg asn arg thr gly met met | 3931/1311<br>CAT GCC AGA TTG CAG CAG CTG GGC AGC CTG<br>his ala arg leu gln gln leu gly ser leu |
| 3961/1321<br>GAT AAC TCT CTC ACT TTT AAC CAC AGC TAT<br>asp asn ser leu thr phe asn his ser tyr | 3991/1331<br>GGC CAC TCG GAC GCA GAT GTT CTG CAC CAG<br>gly his ser asp ala asp val leu his gln |
| 4021/1341<br>TCA TTA CTT GAA GCC AAC ATT GCT ACT GAG<br>ser leu leu glu ala asn ile ala thr glu | 4051/1351<br>GTT TGC CTG ACA GCT CTG GAC ACG CTT TCT<br>val cys leu thr ala leu asp thr leu ser |
| 4081/1361<br>CTA TTT ACA TTG GCG TTT AAG AAC CAG CTC<br>leu phe thr leu ala phe lys asn gln leu | 4111/1371<br>CTG GCC GAC CAT GGA CAT AAT CCT CTC ATG<br>leu ala asp his gly his asn pro leu met |
| 4141/1381<br>AAA AAA GTT TTT GAT GTC TAC CTG TGT TTT<br>lys lys val phe asp val tyr leu cys phe | 4171/1391<br>CTT CAA AAA CAT CAG TCT GAA ACG GCT TTA<br>leu gln lys his gln ser glu thr ala leu |
| 4201/1401<br>AAA AAT GTC TTC ACT GCC TTA AGG TCC TTA<br>lys asn val phe thr ala leu arg ser leu | 4231/1411<br>ATT TAT AAG TTT CCC TCA ACA TTC TAT GAA<br>ile tyr lys phe pro ser thr phe tyr glu |
| 4261/1421<br>GGG AGA GCG GAC ATG TGT GCG GCT CTG TGT<br>gly arg ala asp met cys ala ala leu cys | 4291/1431<br>TAC GAG ATT CTC AAG TGC TGT AAC TCC AAG<br>tyr glu ile leu lys cys cys asn ser lys |
| 4321/1441<br>CTG AGC TCC ATC AGG ACG GAG GCC TCC CAG<br>leu ser ser ile arg thr glu ala ser gln | 4351/1451<br>CTG CTC TAC TTC CTG ATG AGG AAC AAC TTT<br>leu leu tyr phe leu met arg asn asn phe |
| 4381/1461<br>GAT TAC ACT GGA AAG AAG TCC TTT GTC CGG<br>asp tyr thr gly lys lys ser phe val arg | 4411/1471<br>ACA CAT TTG CAA GTC ATC ATA TCT GTC AGC<br>thr his leu gln val ile ile ser val ser |
| 4441/1481<br>CAG CTG ATA GCA GAC GTT GTT GGC ATT GGG<br>gln leu ile ala asp val val gly ile gly | 4471/1491<br>GAA ACC AGA TTC CAG CAG TCC CTG TCC ATC<br>glu thr arg phe gln gln ser leu ser ile |
| 4501/1501<br>ATC AAC AAC TGT GCC AAC AGT GAC CGG CTT<br>ile asn asn cys ala asn ser asp arg leu | 4531/1511<br>ATT AAG CAC ACC AGC TTC TCC TCT GAT GTG<br>ile lys his thr ser phe ser ser asp val |
| 4561/1521<br>AAG GAC TTA ACC AAA AGG ATA CGC ACG GTG<br>lys asp leu thr lys arg ile arg thr val | 4591/1531<br>CTA ATG GCC ACC GCC CAG ATG AAG GAG CAT<br>leu met ala thr ala gln met lys glu his |
| 4621/1541<br>GAG AAC GAC CCA GAG ATG CTG GTG GAC CTC<br>glu asn asp pro glu met leu val asp leu | 4651/1551<br>CAG TAC AGC CTG GCC AAA TCC TAT GCC AGC<br>gln tyr ser leu ala lys ser tyr ala ser |
| 4681/1561<br>ACG CCC GAG CTC AGG AAG ACG TGG CTC GAC<br>thr pro glu leu arg lys thr trp leu asp | 4711/1571<br>AGC ATG GCC AGG ATC CAT GTC AAA AAT GGC<br>ser met ala arg ile his val lys asn gly |

|                                                                                 |           |
|---------------------------------------------------------------------------------|-----------|
| 4741/1581                                                                       | 4771/1591 |
| GAT CTC TCA GAG GCA GCA ATG TGC TAT GTC CAC GTA ACA GCC CTA GTG GCA GAA TAT CTC |           |
| asp leu ser glu ala ala met cys tyr val his val thr ala leu val ala glu tyr leu |           |
| 4801/1601                                                                       | 4831/1611 |
| ACA CGG AAA GGC GTG TTT AGA CAA GGA TGC ACC GCC TTC AGG GTC ATT ACC CCA AAC ATC |           |
| thr arg lys gly val phe arg gln gly cys thr ala phe arg val ile thr pro asn ile |           |
| 4861/1621                                                                       | 4891/1631 |
| GAC GAG GAG GCC TCC ATG ATG GAA GAC GTG GGG ATG CAG GAT GTC CAT TTC AAC GAG GAT |           |
| asp glu glu ala ser met met glu asp val gly met gln asp val his phe asn glu asp |           |
| 4921/1641                                                                       | 4951/1651 |
| GTG CTG ATG GAG CTC CTT GAG CAG TGC GCA GAT GGA CTC TGG AAA GCC GAG CGC TAC GAG |           |
| val leu met glu leu leu glu gln cys ala asp gly leu trp lys ala glu arg tyr glu |           |
| 4981/1661                                                                       | 5011/1671 |
| CTC ATC GCC GAC ATC TAC AAA CTT ATC ATC CCC ATT TAT GAG AAG CGG AGG GAT TTC TTT |           |
| leu ile ala asp ile tyr lys leu ile ile pro ile tyr glu lys arg arg asp phe phe |           |
| 5041/1681                                                                       | 5071/1691 |
| GAA GAT GAA GAT GGA AAG GAG TAT ATT TAC AAG GAA CCC AAA CTC ACA CCG CTG TCG GAA |           |
| glu asp glu asp gly lys glu tyr ile tyr lys glu pro lys leu thr pro leu ser glu |           |
| 5101/1701                                                                       | 5131/1711 |
| ATT TCT CAG AGA CTC CTT AAA CTG TAC TCG GAT AAA TTT GGT TCT GAA AAT GTC AAA ATG |           |
| ile ser gln arg leu leu lys leu tyr ser asp lys phe gly ser glu asn val lys met |           |
| 5161/1721                                                                       | 5191/1731 |
| ATA CAG GAT TCT GGC AAG GTC AAC CCT AAG GAT CTG GAT TCT AAG TAT GCA TAC ATC CAG |           |
| ile gln asp ser gly lys val asn pro lys asp leu asp ser lys tyr ala tyr ile gln |           |
| 5221/1741                                                                       | 5251/1751 |
| GTG ACT CAC GTC ATC CCC TTC TTT GAC GAA AAA GAG TTG CAA GAA AGG AAA ACA GAG TTT |           |
| val thr his val ile pro phe phe asp glu lys glu leu gln glu arg lys thr glu phe |           |
| 5281/1761                                                                       | 5311/1771 |
| GAG AGA TCC CAC AAC ATC CGC CGC TTC ATG TTT GAG ATG CCA TTT ACG CAG ACC GGG AAG |           |
| glu arg ser his asn ile arg arg phe met phe glu met pro phe thr gln thr gly lys |           |
| 5341/1781                                                                       | 5371/1791 |
| AGG CAG GGC GGG GTG GAA GAG CAG TGC AAA CGG CGC ACC ATC CTG ACA GCC ATA CAC TGC |           |
| arg gln gly gly val glu glu gln cys lys arg arg thr ile leu thr ala ile his cys |           |
| 5401/1801                                                                       | 5431/1811 |
| TTC CCT TAT GTG AAG AAG CGC ATC CCT GTC ATG TAC CAG CAC CAC ACT GAC CTG AAC CCC |           |
| phe pro tyr val lys lys arg ile pro val met tyr gln his his thr asp leu asn pro |           |
| 5461/1821                                                                       | 5491/1831 |
| ATC GAG GTG GCC ATT GAC GAG ATG AGT AAG AAG GTG GCG GAG CTC CGG CAG CTG TGC TCC |           |
| ile glu val ala ile asp glu met ser lys lys val ala glu leu arg gln leu cys ser |           |
| 5521/1841                                                                       | 5551/1851 |
| TCG GCC GAG GTG GAC ATG ATC AAA CTG CAG CTC AAA CTC CAG GGC AGC GTG AGT GTT CAG |           |
| ser ala glu val asp met ile lys leu gln leu lys leu gln gly ser val ser val gln |           |

05667837 "1013000

|                                                                                                 |                                                                                                 |
|-------------------------------------------------------------------------------------------------|-------------------------------------------------------------------------------------------------|
| 5581/1861<br>GTC AAT GCT GGC CCA CTA GCA TAT GCG CGA<br>val asn ala gly pro leu ala tyr ala arg | 5611/1871<br>GCT TTC TTA GAT GAT ACA AAC ACA AAG CGA<br>ala phe leu asp asp thr asn thr lys arg |
| 5641/1881<br>TAT CCT GAC AAT AAA GTG AAG CTG CTT AAG<br>tyr pro asp asn lys val lys leu leu lys | 5671/1891<br>GAA GTT TTC AGG CAA TTT GTG GAA GCT TGC<br>glu val phe arg gln phe val glu ala cys |
| 5701/1901<br>GGT CAA GCC TTA GCG GTA AAC GAA CGT CTG<br>gly gln ala leu ala val asn glu arg leu | 5731/1911<br>ATT AAA GAA GAC CAG CTC GAG TAT CAG GAA<br>ile lys glu asp gln leu glu tyr gln glu |
| 5761/1921<br>GAA ATG AAA GCC AAC TAC AGG GAA ATG GCG<br>glu met lys ala asn tyr arg glu met ala | 5791/1931<br>AAG GAG CTT TCT GAA ATC ATG CAT GAG CAG<br>lys glu leu ser glu ile met his glu gln |
| 5821/1941<br>ATC TGC CCC CTG GAG GAG AAG ACG AGC GTC<br>ile cys pro leu glu glu lys thr ser val | 5851/1951<br>TTA CCG AAT TCC CTT CAC ATC TTC AAC GCC<br>leu pro asn ser leu his ile phe asn ala |
| 5881/1961<br>ATC AGT GGG ACT CCA ACA AGC ACA ATG GTT<br>ile ser gly thr pro thr ser thr met val | 5911/1971<br>CAC GGG ATG ACC AGC TCG TCT TCG GTC GTG<br>his gly met thr ser ser ser ser val val |
| 5941/1981<br>TGA TTA CAT CTC ATG GCC CGT GTG TGG GGA<br>TGA                                     | 5971<br>CTT GCT TTG TCA TTT GCA AAC TCA GGA TGC                                                 |
| 6001<br>TTT CCA AAG CCA ATC ACT GGG GAG ACC GAG                                                 | 6031<br>CAC AGG GAG GAC CAA GGG GAA GGG GAG AGA                                                 |
| 6061<br>AAG GAA ATA AAG AAC AAC GTT ATT TCT TAA                                                 | 6091<br>CAG ACT TTC TAT AGG AGT TGT AAG AAG GTG                                                 |
| 6121<br>CAC ATA TTT TTT TAA ATC TCA CTG GCA ATA                                                 | 6151<br>TTC AAA GTT TTC ATT GTG TCT TAA CAA AGG                                                 |
| 6181<br>TGT GGT AGA CAC TCT TGA GCT GGA CTT AGA                                                 | 6211<br>TTT TAT TCT TCC TTG CAG AGT AGT GTT AGA                                                 |
| 6241<br>ATA GAT GGC CTA CAG AAA AAA AAG GTT CTG                                                 | 6271<br>GGA TCT ACA TGG CAG GGA GGG CTG CAC TGA                                                 |
| 6301<br>CAT TGA TGC CTG GGG GAC CTT TTG CCT CGA                                                 | 6331<br>CTC GTG CCG GAA ATC TGA TCG TAA TCA GGG                                                 |
| 6361<br>TAC AGA ACT TAC TAG TTT TGT CTA GGA GTA                                                 | 6391<br>TGT TGT ATG ACT AGG ATT TGT GCT ATT ATC                                                 |
| 6421<br>TCA TTC AAC AAC ATA GAG CAA GAA TAG TGA                                                 | 6451<br>GCT AAC TGA GCT AGA CAC TCA ATT AAT CCG                                                 |
| 6481<br>CTA CTG GCT TCA AGT CAG AAC TTT GTC ATT                                                 | 6511<br>AAT CAT CGA CTC CGG GAC GGT CAT ATA TGT                                                 |
| 6541<br>ATT ACA TTT CTA CAT TTT TAA TAC TCA CAT                                                 | 6571<br>GGG CTT ATG CAT TAA GTT TAA TTG TGA TAA                                                 |
| 6601<br>ATT TGT GCT GGT CCA GTA TAT GCA ATA CAC                                                 | 6631<br>TTT AAT GGT TTA TTC TTG TCA TAA AAA TGT                                                 |
| 6661<br>GCA ATA TGG AGA TGT ATA CAA GTC TTT ACT                                                 |                                                                                                 |

00687837 " 101300  
00687837 " 101300

**A. Allelic variations: single nucleotide changes (polymorphism) between CLASP-2 cDNA isoforms**

| Isoform | Difference   | Nucleotide(s) | Consequence                                                                       |
|---------|--------------|---------------|-----------------------------------------------------------------------------------|
| 1       | polymorphism | 862           | A to G change; mis-sense mutation                                                 |
| 2       | polymorphism |               | A to C change; mis-sense mutation changing codon from histidine to proline        |
| 3       | polymorphism | 2210          | A to G change; mis-sense mutation changing codon from asparagine to glutamic acid |
| 4       | polymorphism | 2225          | C to T change; mis-sense mutation changing codon from histidine to tyrosine       |

**B. Alternative splices**

| Isoform | Difference    | Nucleotide(s) | Consequence                                                                                          |
|---------|---------------|---------------|------------------------------------------------------------------------------------------------------|
| 1       | exon deletion | 209-291       | premature, in-frame stop codon leading to the production of a truncated, most likely soluble protein |

These differences may be found separately or together in various combinations in the different human CLASP-2 isoforms

FIG. 11B

09637837 101300

human CLASP-2

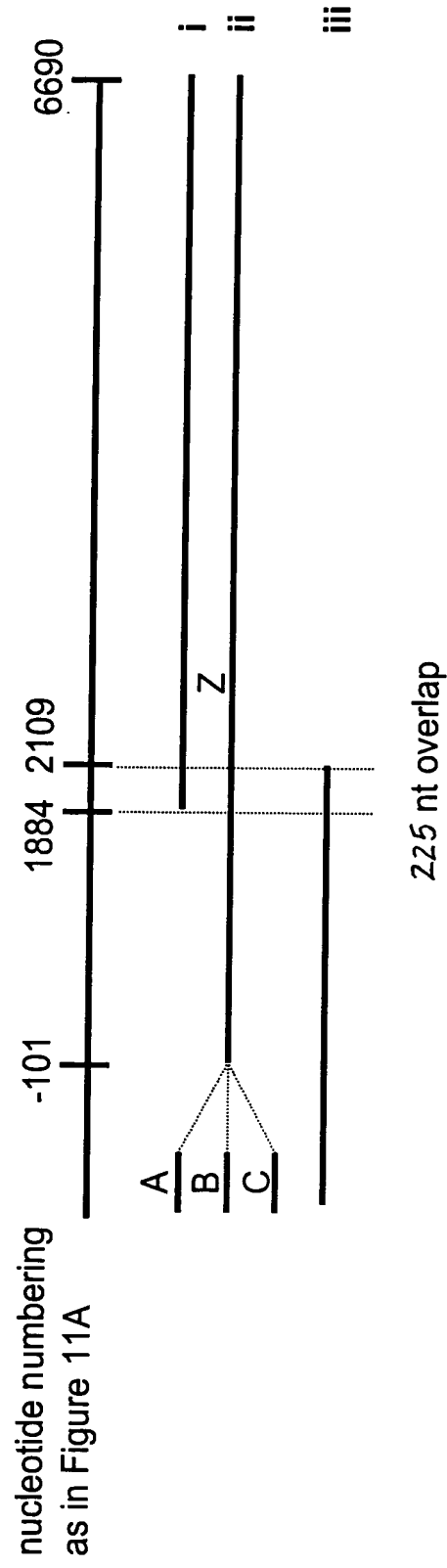


FIG. 11C

1st exon (nucleotides 335 to 445)

TGCTTGCTTATCTTTTCGCCCTCCAGGCAAAGCCAAAGCTAATTGAGCCACT  
CGACTATGAAAATGTCATCGTCCAGAAGAAGACTCAGATCCTGAACGACTGT  
TTACGGGAGATGCTGCTCTTCCCTTACGATGACTTTCAGGTAAGTAACGTTAT  
GTTTCTATCCGTAGAACCACG

2nd exon (nucleotides 7101-7190)

TTACCCAAGGCTTTTCCTCCTGTTTTTGTTCAGACGGCCATCCTGAGACGA  
CAGGGTCGATACATATGCTCAACAGTGCCTGCGAAGGCGGAAGAGGAAGCA  
CAGAGCTTGTTTGTTACAGAGGTAAGGCTCTTTCCTGCATTAATTTACATTT  
GAAGTCATTTTCCCCTAACTGCCTCC

3rd exon (nucleotides 11439 to 11521)

TTTTCTATTTTTTAAAATCCCCCTTCAATAGTGCATCAAAACCTATAACTCTGAC  
TGGCATCTTGTTGAACATAAAATATGAAGATTACTCAGGAGAGTTTCGACAGC  
TTCCGAAGTGAGTAAGCTATATTATACACATAGGGAAAAGTCTTT

4th exon (nucleotides 13987 to 14056)

CTAAACAAATTTTCTTTGTTGTTTTATAGCAAAGTGGTCAAGTTGGATAAA  
CTCCAGTTCATGTCTATGAAGTTGACGAGGAGGTCGACAAAGATGAGGTGG  
GATACCTGCTTGCTGTTGCTTCTCTTTTCACTCTAGATTAA

5th exon (nucleotides 15212 to 15307)

GGAGGTTGACTGCTGGTGTTCCTTCTCTCCTAGGATGCTGCCTCCCTTGGTT  
CCCAGAAGGGTGGGATCACCAAGCATGGCTGGCTGTACAAAGGCAACATGA  
ACAGTGCCATCAGCGTGACCATGAGGGTGAGGACGCACATCACTTTGCCCTC  
CCCTCTCACAAGCCCTTTC

6th exon (nucleotides 16269 to 16404)

TGAAAGAATAGCTGTGTGTATATTTTTCTCTCAGTCATTTAAGAGACGATTTT  
TCCACCTGATTCAACTTGGCGATGGATCCTATAATTTGAATTTTTATAAAGAT  
GAAAAGATCTCCAAAGAACCAAAAGGATCAATATTTCTGGATTCTGTATGG  
GTGTCGTTTCAGGTAAATATGAAAAGAGTTTTACCATTATGTTTTCTTA

7th exon (nucleotides 19459 to 19633)

AAGTATGTCTGTTTATCCTTTTTTTCATTTTCAGAACAAACAAAGTCAGGCGTTTT  
GCTTTTGAGCTCAAGATGCAGGACAAAAGTAGTTATCTCTTGGCAGCAGACA  
GTGAAGTGGAATGGAAGAATGGATCACAATTCTAAATAAGATCCTCCAGCT  
CAACTTTGAAGCTGCAATGCAAGAAAAGCGAAATGGCGACTCTCACGAAGGT  
AGATAGGCTTGGCTTCCCCCAGGCACATACACACTCT

8th exon (nucleotides 20567 to 20634)



ATTACAAGTGATTCCGATAATCTGTTTTGCCATTTTAGATGATGAACAAAGCA  
AATTGGAAGGTTCTGGTTCCGGTTTAGATAGCTACCTGCCGGAACTTGCCAAG  
GTAACATCGTCTTATATCTTCTGCTCTTCGTTGAATGC

9th exon (nucleotides 30257 to 30331)

GATTGTGTTAAATGTAATTTTCATGTATCTTGTTATCAGAGTGCAAGAGAAGC  
AGAAATCAAACATAAAAAGTGAAAGCAGAGTCAAACCTTTTTTATTTGGACCCA  
GATGCCCAGGTAAGAAGTATCTAAATGTTTAATATTTAAAACCAAAT

10th exon (nucleotides 31851 to 31991)

CATAACTTATTTATATGTTTACATTTTCTTTTAAAGAAGCTTGACTTCTCATCA  
GCTGAGCCAGAAGTGAAAGTCATTTGAAGAGAAGTTTGGAAAAAGGATCCTTG  
TCAAGTGCAATGATTTATCTTTCAATTTGCAATGCTGTGTTGCCGAAAATGAA  
GAAGGACCCACTACAAATGTAATTTTTCATTTTAAAAATAAACATTAAAAAA  
AAAATAGGCAG

11th exon (nucleotides 32472 to 32675)

CCATGGTGATCATTGGATTGTTTTGTTTTGTTTCAGGTTGAACCTTTCTTTGTTA  
CTCTATCCCTGTTTGACATAAAATACAACCGGAAGATTTCTGCCGATTTCAC  
GTAGACCTGAACCATTTCTCAGTGAGGCAAATGCTCGCCACCACGTCCCCGG  
CGCTGATGAATGGCAGTGGGCAGAGCCCATCTGTCCTCAAGGGCATCCTTCA  
TGAAGCCGCCATGCAGTATCCGAAGCAGGTGGGGAGTATGAGCCCAGCATTC  
CCACTACTCAGACTCACTTTGCATGC

12th exon (nucleotides 33063 to 33185)

GAATTCTGCTTACTGAAGAAAATTGTTTGCCTCCTAGGGAATATTTTCAGTCA  
CTTGTCCTCATCCAGATATATTTCTTGTTGGCCAGAATTGAAAAAGTCCTTCAG  
GGGAGCATCACACATTGCGCTGAGCCATATATGAAAAGTTCAGACTCTTCTA  
AGGTATGAATGGCTTTTACGCTTTGGGGTGGTAAAAAGCAATCTGAA

13th exon (nucleotides 36702 to 36784)

CAGTATCTCATAGCTTTATTCTCATGTCTTCAAGGTGGCCCAGAAGGTGCTGA  
AGAATGCCAAGCAGGCATGCCAAAGACTAGGACAGTATAGAATGCCATTTGC  
TTGGGCAGCAAGGTAAGGAACACCTTTTATACCTTTTAAATCGATATAGATA  
GGTGCATGG

14th partial exon (nucleotides 37353 to 37475)

GAAACCCAGTTTAGAAATGTTGCTTTGCCATTTTCAGGACATTGTTTAAGGATG  
CATCTGGAAATCTTGACAAAAATGCCAGATTTTCTGCCATCTACAGGCAAGA  
CAGCAATAAGCTATCCAATGATGACATGCTCAAGTTACTTGCAGACTTTCGG  
AA

1 TACCAAGGGCAACTCTGGCACACCCATAAGTCTGGAAAGGGGACATAGCTAGTCAGGGATGACCCGAGAAATGACTGGAAGCTCCACCAGAA  
93 TGCAGAGCTTCCTTTGTGCTTAAATAACTGAACAAGCATCACTCTGTGTAGCAGGACACCACCCAGCATTTTTTGTCCCTTTGGAAACAACT  
185 CTTATTTCTGTTTCTTTGTGATACAAAACCTAGCATACTCTAATTGTAGAAAATACAAAACATAGAGTAGAACATACTAAGTTCTTTATCTT  
277 AAGAAATGGCATTGTGTATGAGAATGCTTGTCTTATCTTTTCGCCCTCCAGGCAAAGCCAAAGCTAATTGAGCCACTCGACTATGAAAATG  
369 TCATCGTCCAGAAGAAGACTCAGATCCTGAACGACTGTTTACGGGAGATGCTGCTCTTCCCTTACGATGACTTTCAGGTAAGTAACGTTATG  
461 TTCTATCCGTAGAACACGTTGTTGATCTTAACAAGCAGTATTTTTCTATGTATTGATTTATTGTTTGGTTAGTTAATTATTATTATTATT  
553 ATTTTTTTTGAGACACAGTCTTGCTCTGTACGCGAGGCTTGAGTGCAGTGGTGCCATCTTGGCTCAACGGCAACCTCCGCCCTCTGGGTTCA  
645 AGCATTCTCTGCTCAGCCTCTCAAGTAAGTGGGATTACAGGCGTGTGCCACCATGCTGGCTAATTTTTGTCTTTGTATTAGAGACAGG  
737 GTTTTGCCACGGTGGCCAGGTCGTCCCAAACCTCTGGCCTTAAGTGATCTATCTGCCTTGGCCTCTCAAAATGTTGGGATTATAGGCATGA  
829 GCCACTGTGCCCCGCCCTAATTATGGTTTTTAAAGATGAAAATAAGATGTTATTTAAGAAAGAAAAGTTATTTTATATCTTCCAAGCATCC  
921 TTCATGAGTTGATAATTTTAAATGGTATATTTTTGCATATTAATTTATAAGTATGCCAAAATGTGTGTGTGTGTGTGTGTGTGTGTGTGT  
1013 GTGTATCTTGAATAAAAGTCTATACCTCTGTCTGGGCTGATTTAGTGGGCACAGTGCCCTTTCTGTCTTTTGAGATTTGTTTTGATTAGAT  
1105 TTTTGGCCAAAGTACCTTAGAATCTTAATGATGGGCTTTGCTGGGGAGCAGTGGGAGATTTCGTCTATGCCCTTTTTTTAGGATGGCATTTGGG  
1197 AGCCTGCCTTCAGAGGCCCTGCACCTCTGTGTGGGCTCCAGCAAAGCGTTCAAGGTTAGCCAAGAATGGCCTGAAGTTTACCTCTGTAGTGT  
1289 AATGTGGGTGCTGTTCTTGGAAAGAAATGTGGAGGACTCAGCACAGCTCCTGCTGTGTGCCGCTCTTTCAGGCTATGGCTGTGGTTAAGAG  
1381 ACTAACAAGAAGCTGTGAGGCTGTTGAGGAATGAGAATGACATCTTCTCCAGGAAACCCGGTGGTGTAAATGCCCTGCAGCGAGCCACC  
1473 TTGGTCCATTGAGAGGTTCTGGTTACTTTCTTGTCTCTCTGGGACCTGATCCTGGCATTCTTTCTCCTCTCCTTTGATGCTCTTAGTTGG  
1565 ACACCTCTCTACCTGATGCTGTTACCATTTAAGCCCTGTCTTTTGTGAATCGAGCTGCCCTTTTTTTTTTAAGCTTCACTGATTCTTTGTGT  
1657 TTGATTCCAAAAGTGTTACATCCATGTACAAAAAGATAAATGAGAGGGAAATATTGAAATAATTGACATGAAAAGCCTCCCCAGCCTTCTA  
1749 ATCCCATCCACAGAACATGACTTAACTGTATACAGCTCTGTGCATACTTGTCTTTAGAAACTTCCATGTTAATAGAAATTGTTAAATTACG  
1841 ATCCTTGAAGGTTTTTCCACCAAATTTAAGCGACTCCAGCTTACAACAGAGGTGAGAATTTTCAAAATGTTCACTCTTTCTAACTTGT  
1933 AGAGATACCTGGGCCCCAAATGATTATCTTTAGCTCTGTCTGCATAAAAGGAATGCCATGGGAATGAAATTGACCATTCTGTGGTGT  
2025 TGCTACCAAAGTAACAGGTAAATGGGTTGAGGTCATGCCAAACAATACCATGCTTTGCATACTTCATTTTCATGACTAACTGCATGGGAACG  
2117 GACTAATAAATGAGAACCCTCTGAATGATGCCCTTTGCTGTGATTTGGCAACAAATGAAAAGCAAATCAAATGATTATAAATGTACTGCA  
2209 TGTGACAAGATTTCTCTGTAGTGTGTCTGAGGAAGCTAAAGGTTATCTCAAATTTCTCTCAACATGAAGTATGTGTCTTCTTGGTATTA  
2301 ATTAAGTAACAACCTTTTTTGTGTTGCAACCTAGAATGAAAAATCTAATTGTATGACTGAGATAAAATTGCTTAAGAAACAACCAAAGAA  
2393 ACGAGATACAGTTAGTTGAGTGTCTATCTTTATCCAGGGAACAGGTATCTGGATGTTTAAGCAGTTGCAGAATCAGACAGTTTAACTTTGA  
2485 GAAAACCTCTGTGTCCCTTTGCTTTTAACTACTCTGGTGATAGCAGGCACAAATATTCTAGGAAAGGCAAAGAACTCACTAGCATTGTT  
2577 GGCTAAGGTGATGAGCAATATATTCTTCTGTTTGGGGAGAAGTTTCTTAGAGATTAGGAGCTTGAATTGGAGCTTTAATCCTCATCACA  
2669 GGAATTGTGATGGGCCCCAGTGAAGTTGGGTACAATTATTTGTTTCTTATAGACTCCCACTTTCTTATCAGGTAAAGCCATGTACTCTGT  
2761 GCTTCTTGTAAATGTCTCAGTGATGTTATTAAGTGTCTAATTAGCTGGATGAGTGAAAGGTCTTAACAGTGCCACAGATTCTTTCTATC  
2853 TGTGTTTTCTTAGGCAGAATAAGAGCAGAATTATTGTATTATTAGAGGCAGAGGGAACAATTAGATTGGGGAAAGTGTTTTATTTCATATG  
2945 GAAAAGTAATACCAAGTTGGTTAGGAAATGGCAGCAGCAAAACGCATGCTGAGGGGTGATTACTGCACTTAAATAATTTAGCAGTATAAGT  
3037 TAACATATAAATAATAGAACTTGGTGTCCATTTCTGCCAAATATATTGAAATGACAATTTACTAAAATATAAGCATGGATAGTGGTGATG  
3129 CTTGTGTACATTTTTCAAGTAGGCACATGTTGATCTTGAGCCTTACTGGTCAGATCCTAAAGGCATCTACATGTTCTCTAAAAATGAGTTG  
3221 TGTCAGAAAAGATTGCGGGTTGCATGTAGTTGCCCTGAGGATGACAGAAGAGTAGTTACTACAACAGCAGCAAAGAAGAGACATGAAGT  
3313 AAACGTGGATTTTTAAAAATCAAAAGAATAGGCCAGGCGCACTGGCTCATGCCCTGTAATCCAGCACTTTGGGAGGCCGAGGTGGGCAGATC  
3405 ACAAGGTGAGGATTTGAGACCAGCCTGGCCAATATGGTGAACCCCATCTCTACCAGAAAATACAAAATTAGCCAGGCATGGTGGTGCATG  
3497 CCTGTAATCCAGCTACTCGGGAGGCTGAGGCAGGAGAATCTCTTGAACCCAGGAGACAGAGGTTGCAGTAAGCTGAGATCGTCCACTGCA  
3589 TTCCAGCCTGGGCGACAGAGTGAGACTCCATCTCAAAACAAACAAAAATCAAAATAATAGTTCCAGCCATCAGGTTATTGATGAAGTAGG  
3681 CTGGGCACGGTGGCTCACACCTGTAATCCAGCACATTGGGAGTCCGAGGCAGGTGGATCACCTGAGGTGAGGTGTTGAGACCAGCCTGGC  
3773 CAACATGGCAAACCCCGTCTCTACTAAAAATACAAAAATTAGCCAGGCATGGTGGTGGGCACCTATAATCCAGCTACTTGGGAGGCTGAG  
3865 GCAAGAGAAATCGCTTGAACCTGGGAGGTGGAGGTTGCAGTGAGCCAAGATCGCGCCATTGCACTCCAGCCTGGGGGACAAGAGGAAAACCTCC  
3957 ATCTCAAAAAAAGGGAATATTAATGAAGTAAAGTACATGTGATCTGCCATGGCCAGGACAGGAATGCCATGGGGCTGCAGCCGTCA  
4049 CTAGCTGATGGCCCTTCTTTTTGCAAGATCAGATCCTGTGCTTGGGGATCTCTGCCATCTGTGCTTTGGCTTCATGGTTCTCCTTGCCAGC  
4141 AGCATCTTCTCTTAGATCTTTCTTACCCTTTAGAGACCCTTGAATCCCATATTGTCTGAAGCTATTTAAGTCCACAGAACTTTTCCC  
4233 CCCACTGTCTCAATTCTTTCTTACTGCTGTCTGCACCGTGCACATAAACACTTGAGTATGTGGTCTTGGCTGTTACGACCTACTTCTTA  
4325 GGCTTCTTGCACGCAGGCATCCCGCCCGTGTGTGGTCTGAGAAGGGCTGGCTTTGAGCCTCTGTTCTCCACCCACCTGCCACCTACA  
4417 CATGCACAAAATCCCTTTCTTGCTAGGTGCTAGGTTGAATACCCATTGCTTACCTTACTAATAGTAAAAATTTTACAAGCATTAGGTTATT  
4509 TTCTTTGATTCACTAAGTAAATATTAATACTGTTTGAACATGTGATAGTCCAGCGACTAGATTGTAAAAATATTTGCAGGATCAATGAT

FIG. 12B  
1 of 10



9201 GGGTGGGGGTTGCTTGCCCTAATTCTGTGCTTCTGCTTTGGAATTTAGCCAATGCCTGCTATGTAGATGGTCAACACTGGCTTGTAAATCAA  
9293 TGAATCTCTAAATACTTAGCCAGGTTCACTGTGGAGTTTTTTTTTTGTTTTTTTTTTTGTATGTGCGATTCTTATAATTATAAATATA  
9385 TGAACATAATAAAGTGAATTATTTTCCCATTTTGCCTAAGGTAATAAATCTTGGCCAGGCGAGTGGCTCACGCCTGTAATCCAGTAC  
9477 TTTGGGAGGCGGAGGCGGGTGGATCAGGAGGTGAGAGTTCGAGACCAGCCTGACCAACATTGTGAACCCTGTCTCTACTAAAAATACAAA  
9569 AAGTAGCCAGGCGTCGTGGTGTTCGCTGTAATCCAGCTACTCGGGAGGCTGAGGTAGGAGAATCGCTTGAACCCGGGAGGCAGAGGTTGC  
9661 AGTGAGCCAAGATTGCACCCTGCCTCCAGCCTGGGTAAACAGAGCAAGATTCCGTCTTAAAAAAAATAAATAAATAAATAAATAAATCTGGG  
9753 CTCCATTCTATAAATGCATTATAATATACAAATTTATGCTGGTTTATTTAGTTTAAATTGGGCAGGTACATTTTATACTTCAGAATAGTTT  
9845 TAATGTCCTGCAGGAGACTTGGTGGTACAAATTCAGTTCTAGAGCTTGTGAAAAACCGCTGTAGCTCTTTGAAGAGAATAGGATCACACCC  
9937 ACAAGACCAGCTCGTACATAGTCAGGCTGACTACTTAGCTGTGCCAGTGGACCTAGGGGCAGTAGTGGGAAAATCCTAACTATGGATTAT  
10029 TCTGAAATCTGACTGGTTTTGGAATGAAATTTTGTAGTGTGAATGTATGATACTCAAAATGTGAAATGCTTTGAGAAATCTAAAAAATCAT  
10121 TTTCAAGGATAAAATAGCATTTTAAATATTCTTAACACAGAGTAAAAAATCAAAAAGTTTGCCAGCTCCAAAATCTGACTTTGCGCTTA  
10213 GCCCTTCTCTGCCATTTATCCACCTCTCAGAATAATTTAAAACTTACATTACCTTCACATCACACATCACACCCTTGCCAGTAAAGTGC  
10305 TTATTGTAGAGCTTGGCACAAAATAAGCACTTGCTGCTGTTGTAATCTTACTTTTCATGAGTTTGGAGGTGGAGGGGAGTTGCTTCAGAAG  
10397 ACCTTCAGGCATGGCCTGTGACACAGATAGAAAGGTTGACAGTAGAAACGATGAAGTGAAGAAGCAGAATAGAGACGTTGTTTCATGTTAGT  
10489 TACAGCCAGAGCCAAATAAAGTAGATAAGGCATAAATACATTTATCGACCTATGTTTTCATTGATTCACTCATGCTTTTTTCCACCCACAC  
10581 TGAAGTCTGCACATAAATAGTCAAGTGTGACTGGACAGAAGATCATTGAACTAAGCTGATTTTAACTAAATCTTTAGCTTTTGATTTT  
10673 GACTCATTCTATTTGAAGATCTGGTGGATGTGGCATTATAATCTTAGGCTTTATGCACTATTGGAGGATCTTCATGGGTGGATGAACGACG  
10765 GACACCAGGCTGGCCCATTTGAATCTGTCTGTGCGCAGGTAGTTTGAATGCAGTCTGTGTAGGTGAGGTCACTAATAGAATCCTTGCCAGTG  
10857 GAAGACTACATTAAACATTCTGTACACACACAGATGAAATGTCATGGTGCTAATATTAATTGGAATGCATATGTTTCTTCTTAATTATT  
10949 TCACTCTTTTCTTATGAATGAAAGAAAACTGAGGGCAGATTATATGGAATATTAACACAGAGCTAGCTAGTTCTAATATTAGTAA  
11041 ATACCATGAAGCGCTCTTAAGTTCACGCATCCTATTCACTTTTATGTCTAGTAGAGGCCACATGGCTTTTAAAGAACAGGTGCTTACTC  
11133 TGAATAGTCCATTGTTAAGTAAATGTCACAAGGTTAGGTGAAGTTGTCTCCTTGTAACCTGCTCTCAGATCATTAATGATGATAACTTA  
11225 AAGTGATACTACCCCAAGGGTAATGTTTCAGTGGTTCAAAGTCTCAAGCTTCACAGGAATCTCTGGTGGTGAATTTAGGCATTAGCTCG  
11317 TTGATGGGAAAAAATTTTTTGATGTTTCTATGGGTATGCCTTCACAACTTTCCCAAGTGTTTCCAAAAATCACGCTTTCTGTTTTTTA  
11409 TTTTCTATTTTAAATCCCCCTTCAATAGTGCATCAAACTTATAACTCTGACTGGCATCTTGTGAACATAAATATGAAGATTACTCAGG  
11501 AGAGTTTCGACAGCTTCCGAAGTGAGTAAGCTATATTATACACATAGGGAAAAGTCTTTGTACTTGAAATGCTTGGGGGAGGTATGTAAT  
11593 TCATATGCAATCAGAGTAATTGAGGAAAATATTTTTAGATGGTTATGTGTATGTGGTGTAATATTGTTTACAGGGCCTTTGATTGTAAGA  
11685 CTCAAACATGCTACTTTGGTAITGATAGGTAGTAATAAACATGTGGATGGTTAATTATGTCCAGTGGTCTTTTCAGGGTACCCTGATAA  
11777 ATAAATAGGTGAAATTTTTTCACTACAAAATATAAAACAAACAAACGTAAGTGTACTGAAATATGCTGCAGTGCATTTTTCTCTGAAAAG  
11869 AATAITTTGAAGAAGATAATTATAAAGAGCATTTTACATTGAATAAATTTATGTTTTTAAAAAAGTAATCAAGAAACAAGCATTTTCCC  
11961 AGTTAAATTTTTTTTTATCTCCTTTAATGTATTAACCTTATCTAGACTATACAAAAGCAAGTGTATTTAGATTGAATAGTTGTGGCCAAA  
12053 GTGAATCGCGGTAGCTAGGTATTGCCTTGACAGACTATCTTTTATAAAGGTTCCATTGTGTGTGCTTTAAAGGAATACCTGAGACTGGGT  
12145 AATTCTTAAAGAAAAGAGATTTATTTATTTATTTATTTATTTAGTTTTGAGACAGAGTCTTGCTCTGTCAACCAGGCTGGAATACAATGA  
12237 CACGATCTCTGCTCACTGCAACCTCCACCTCCCAAGTTCAGCAACTCTCCCGCCTCAGCCTCCCGAGTTGCTGGGATTACAGCCACTTGCC  
12329 ACCACGCCCGCTAAITTTGTATTTTAGTAGAGACAGGTTTACCCTGTTGGCCAGGCTGGTCTCGAACTCCTGAACTCAGGTGATCCAC  
12421 CTGCCCTCTGCCCTCCCAAAGTGTGGGATTACAAGCATTAGCCACCGAGACTAGCCAAGAAAAGAGATTATTTCGCTTATAGTTCTGCAGGT  
12513 TGTACAAGAAGCATAGCACTGGCTCTGCTCAGCTTCTGTTGAAGACTTTTGTGCTGCTTCAAAACATGATGAAAAGGTCAAAGGGAAAGT  
12605 TGGCACTTGTGAAAAGAGACCAAAGAGGAGGAGAACTCACTTTATAACAACCCATTCTCTTGGGTACTAATCCATTTCAGCAACAAGTAA  
12697 TCCCATCTTGCCAGGAACAAGATTCACTCATTACTGTGAGAACAGCACCAAGCCTCTCATGATGGATCTGCCCCATAACCCACTAGGCCCA  
12789 ATTATGCAACAACGGGGACCAATTTCAATCTGAGTTTGGTGGGAATAAAAACCATATCCAAACCATAGCAGTTGGCAAATTGAATTATAC  
12881 TTGATTTTGGGAAAATTGAAAGCAAATAGTGATGGATTATGTTTTAAACTAACCATCACCAATGAAAATATTACTTGAGACCTGATTAAATG  
12973 TATTTTTCTTTGCGTTTGTACATCTTTGAGCTGGAACCTTTATGCGGTTCTCAGTAGACCTAGCTGTTTGTTTTTCTCCTCTGTGTGGCT  
13065 TTGCCACTCCTTAAGAAATGTTGCGCAATTTCCCGATTGCCTCTTTTTAAACCTCAGCCAGGAACACTCCCTCCTAGTATTATCTTCTCCAG  
13157 ATGGGTAGCCCTTTAGTTCTATATTTACCCAATCCTCCCTTAGGGATTTTTTAAITCTTCCCATTTGGATTGGCTTAACCATCTTTGTTGAT  
13249 CCTCTTGTTCATAGTCTCAGGGTTGAAGATATCAGACTATGTCATGTCGTATACTTACTATCTAATAGACTGCTGGTACATTTCTCTCTT  
13341 GGCATTAAATGAGAATTTCCAAATGTGTGATGAGAAAGAGAGGGAGAATTGTAACAGTGGTGAAGAACACAGATTCTGTGTTCTGCCCTCAGAC  
13433 GACTCTGCCGTCTGTGAGCCTGATTTTCTCATCTGTTAAATGGCCTTAACAACAGTCACCATGATTAAAGGATTAAATGAGAGGGCAGATG  
13525 AGAAGTGCAGGCGCTAGCACGTCAATCCCAITGAGTAAATGTAAGCTGCTTATGGTATGGTGTCTGTTTTGTTGTGGTTAATACCA  
13617 TCATTGTTAATCGGTTTCAACGCAACCACTCAATCTTCTTTTTTCTCATAAATTTGTATTAAGGTTATCTACCAAGTCTTTGTTTAA  
13709 TAAAAACTAATCCACTTTCTATTTTATGATGCTTAACTCCCAGAGCTATGCTGTCTTTTCCACATAGCTTTTTGGAGCTTTCTT

FIG. 12B  
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13801 ACTCAAGTCTCTTGGCTTACCCACCTTGAAAAGCAAGGGCATAGATGGTTTATTCTTTGTCTGAATAAAGAGCTGGGCCATCTTTGGATT  
13893 TAGTAAAGGCCGGGCCCTATGATGGAGGAAGAAATGCAAAGCCTCTTCCTTGACTAGGCATTTCTAAAACAAATTTCTTTGTTGTTTTAT  
13985 AGCAAAGTGGTCAAGTTGGATAAACTTCCAGTTCATGTCTATGAAGTTGACGAGGAGGTCGACAAAGATGAGGTGGGATACCTGCTTGCTGT  
14077 TGCTTCTCTTTTCACTCTAGATTAAACATCAATTTTACAGACTTAGAAGATTAGTTAGAAAATTACCGACATTTAGCCAAAACAGGCATTG  
14169 GAGTGTACATGAAACGGGAATAATTTTTTAAAAATGTTATTGATTGATTGGAATAAGGTCTCTGTTTCACTTTACTGCTTAGCATTTTCAT  
14261 GTTCTCTTGGTTGTGTTTATTTGTTCTGAGATCATTTTCAAAGACTTGGATCAGATCTGGCTACATTGTTAAAAGATATCAAGATGACTTAG  
14353 ACCTTGAATTTAGGTTGTTTTC AACAGATCTCGAAACAGCTGCCAGCCAGTAGATTAAATGGCTATTCTTCAATGATTGCTTTTAGTGA  
14445 AGTCTGATTTGATCAAGCCCACTCCCCCTATTCTAGAGGAAAGCTCATGGCTAAAGAACTATATAAAGGGAGTAGGGCATTGAGATGAGTC  
14537 TGCCCACTGAGTGAGGGAACCTCACAAGAAGACAATGCCATCTCTGCATTTCTCATCCTCCCCATTGATTGTTAAGTGTCCCATTGTGAG  
14629 TTTAGGTTTTTCTCTCTTAAAAAAATGTGACGTGAGCTATAACATTAGCCACTCATTAAAGCAATGTGCATGTAGCAAATATTTTTATTCT  
14721 CCCCATCACTTTATCTCTCTCTTCTGTATTGCTCAATTTCTCTCCCTTGCTTTATTACCTTTCCCTGAACCTAGCCCTCTGGGAAGGTTTC  
14813 CAGGAATGTGCATGTGCTTTTGTCTCTGACTATAGGGGAGTGTCAATTTGAAAACATTTTTTCGTGAAACCAGGCAAGACCTTCCAACGTGA  
14905 GTGGTCAGTTGAGGTATGCTTTTTTGGTCCTTTTGTGGCTCATTAAACACTGACAAATAAAAAATTTGGACAGGAGCTAGCTTTGCCCTTTAA  
14997 TGAATAAAGTTTTTCAGAAATGTAGGCGGGTCTCTCTTTTACCCTGCTAAGTGGACTTTTATGTGACTTGTAGGCATTGGTGTCAATGGGTG  
15089 CTTCAAGTAAAGGGCAATGGACAACCTTGGCACAAAGGGAATGACCTTCCCATTGACCAAACCTCACAGCAAGCAACCAGGTAATAACGGGAG  
15181 GTTGACTGCTGGTGTCTTCTCTCTCTAGGATGCTGCCTCCCTTGCTTCCCAGAAGGGTGGGATCACCAGCATGGCTGGCTGTACAAAG  
15273 GCAACATGAACAGTGCCATCAGCTGACCATGAGGGTGAAGACGCACATCACTTTGCCCTCCCCCTCTACAAGCCCTTTCTGCCATAGAGCT  
15365 CGAGAACAATGCTCAAGATGAATGCGCATGCTGTTCTTCCCCACAAAAGGGACATTGTCTGATTCTAGGATGCTCCCCCTGGTGATAGCACC  
15457 CCCATTGGCACAGCTCATCCACCCACTTTCCCTCACTGTCTTCTGACCACCAGCATAAGGAGACCATCCCTGGGCTGGTGTGAAGGTGCAG  
15549 ACACTGACATAGGCTTTCTCTCTGTAATAACTGAAAAGTGCTCTTTGGTACCTCACAGAATGTCAACAGGGGCTATCTGTATGCCAATC  
15641 CTGAGCACTTCTGTGGAGGTGACTGACGACAAAGTCAAGTAAAGCAAAAATTGAGGACGAGAAAAGAAAATAGTTGCATAGAGAGAAGGTT  
15733 GCAGACAGAGAAGTCAAAACATAGAAGAAGCTATTCAAGGAGAAAAGTGGGACCAGAGGAACATCAGGATTAATAACAAAGGGAAGAGAAAC  
15825 AAGGGAGTCAGGGAGATAAAAATTAAGGAGGAAATGTGACTGTCAATTACCTTAAGGCTGGAAAATCATTCAGCGTCATGAGGCAAAAATAG  
15917 TTCCCATTTCTGTGAGCAAGAAACCTGGGGATTTTAGAGAAAGTTCTGTCTCTCTGTGCTGCATCCCAATTTGGAAGTCCCTGCACTGCTT  
16009 TTGGGTAGTTATGTAAAATCTCTGATTCCGTGGGTGAGAAAATGACCCATGGATATTAGGGGAACCACCTCCTCAGAAGTGAATGCAGTG  
16101 AGCTTCTTAGATGGGATGGGGAGTCTTGACCCACAGTGACCTGGAGCATCAGCTAGAGTGAGAACGGAACAGGTTTTATGTATGTATGTA  
16193 GTCATAAGTGGGTTATTGATAGAGATTGTGACCTCTTCATTTTGAAGAATAGCTGTGTGTATATTTTTCTCTCAGTCATTAAAGAGACGA  
16285 TTTTCCACCTGATTCAACTTGGCGATGGATCCTATAATTTGAATTTTATAAAGATGAAAAGATCTCAAAGAACCAAAAGGATCAATATT  
16377 TCTGGATTCTGTATGGGTGTCGTTTCAAGTAAATATGAAAAGAGTTTACCATTATGTTTCTTATCTGCAGTAGTGCTTATGTGTAAATTA  
16469 GCAGATTTAAGCAAACACTTCCAAAATGGCAATATGCATGGTAGAAATATAACATATAACTTTAAATGAGGCAAGCCTTGTTTTTCATCAT  
16561 TGTAGAAGATGGAAGGATAATGTAGAGGCAGAATTATGCTGTGGCAGGCAGGAGCACTCTGGCTCGGCCACTTTATAGCTGCGTGACCTTT  
16653 AACAGGCTACTTAATTCAGATAATGAGAATGTTTCTTAAATACGGCAAATGAGTACATTGGATGAATCAGTGCAGGAAAATATTTAAACAC  
16745 TTCATAGTATCTCAGTGGTGATTTTTATCGCTAGCATTGTAGTACCAGTGGCGGTGTAGATCAGTAAAGAGATTAGGTTTCAGCGCAGATTG  
16837 AGTTCAAATCCCTGCTCCTCCACTTACCAACTGTGTAACCTTGAGATGTTATTTAACCTCTCTGTACCTCAGTTTCTTCATTTGTTAAATA  
16929 AGGATAATGGCAGTACCAATATGGTTACTGAGAGGGTTCATTACATACATGTA AAAAGCTTAGAACAGTGCCAACAAATGGTAAGCATT  
17021 TGGTCAGTATTAGATAGTTTTGTTATCATAGGGCTGTTGTACTTTTATATCATAGGGCTTATGTACTTATCCTTTAAAATTATTGTTAATTA  
17113 AAGATAACACATGAATGTATTTTTCTTGTA AAAATCAGCCAATACAGATAAAGTGAAGTCCCTTCTGGACTCCTCCCCCTCCTTCAGTGTCT  
17205 CTTTTCTGAGGGGAGCTACTACCAGTTTTGCATGCATCCTTCTGTAGCTTTTTAGCATTGTCTTTGGAAGAGAGTTGTCAATTTCCCTGTCC  
17297 ATCATCTGTCCATCCATCCATCCATCCATCTGTCCACCCCTCCATTTCATCCAGCCTTGCCACTTTCAAGGAAGATTTAAGGCAGCAGC  
17389 TTATAAGCATACACAGGACATGGGATAGCATAAATTTAAAGTGGGGGTGAAAGCAGAAAGATGAACAGGGGATTGGGATAAGGGTGAGAGAA  
17481 AATAGAGTTAAGGAGAAAGCGTATGTTTTGAAGATCTAACACCTGCTGTGGGTGGGCCACCACCTGGGCTCTATGCTTTCTCACTTGAGAGC  
17573 CTGTTTAGTCACGCAATTCACAGTGCACATGAGATAAAGGCATGATGCCTGTTTAGTCGACTCTAGAAGCACCCCTGACTTTAAAAAGAAGT  
17665 TAAAGCAAACCTAAATGTATTTGGCAACCTCATTTTTTAAAGTAGGAAGTAATTATTTTTGTTTTATAAGAGAGTTTTGCTGCCTGTTCTG  
17757 GCCCAGGGACAGATGTTTATAAGTACAACCTGCCTGAGCTATCAATTAGTCTCCGGGTGCATTTCAAATCTAAGGTTCTGACTTCAATGG  
17849 AAGTCTCTCTCTCAAATGTCTTTGCAGATGCAGCTGATGGTGTTCATTTAATAAAGTGATCCAAGGCTTCAAAAAGTAAAAATAATT  
17941 TGTTTTATCTGTGTCTGTTTGTA AACTAAGCATCAAAAGTTGTGATTAAAGTGTTTTTAAAAATTATTACTTATGGATATTATAAAAAAAT  
18033 TAGTTGACTGGTGCTGTGAATTA AAAAAGTGCCATAA AACTAAAAAATTTGAAGCATTTTAGAACCTTGAAATTTATTATACTTATTTTGC  
18125 AGATGAGAAAACCTGAGGCTCAGAAACAGAAATTTAGAATTGAGGCCAATGTTTTTTCTCCACTTTTAACTTTCTCTTTTCATGATTGTGA  
18217 GTATGCAGGGAAAGGAGGAGAGAAATTCATTTGTTTCAAGCCTTTGACTTCTTCCCTGGTCTTGCCCTGAAGTTAAGTGGAAATCCAAA  
18309 GTGCAATTACTGAGCCACAGCAGACAGTCTGTGCACAAGAGTGTGTGGCTTTGCCAAGGGGAGCACTTGACTTTGCATTTCTAAGAAGCTG

FIG. 12B  
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18401 TGCTGCAGAATCACAGAGACTTTTGGGAGGGTTGCCCTGTCCCTGAGACCTCCACCAAGGAACCTCTTAGAGAGAGTGTGGATAACCCAGTAG  
 18493 GATTTTGTAGTGGCTATGCGGGGGGCTGTCTGTGGCTCAGGTTAGTGGGAGTGTTCATATCGCTCAGCCTGTCTTACAGGGGATC  
 18585 TTGTGCCATGATCCTCAGAGCTGAACCTCTGTCTACTGCGGCCAACCTGGGGAGATTTTGTCCCTGGAGGACATCTTGGAAATGTCTGAAGA  
 18677 CTGGCATCTATTGGCTTAAGGCCATAAAATTCGCTAAACATTGTACAATGCATGGACCAGCCACTCACAACAAAGAATTGGCTGCCCAAGTG  
 18769 TCAGTAGTACCGAGATTGAGAAATCCTGGCCTAGTGCATGTTTCATCTTCCGTCTGTTACTGCACATGGACTACTGTTCTTGTCTGTGAGCC  
 18861 AGTCACCCCTCTTGCAGGCATGAAAACCTGGAGGCATGAGGCAAGGCCACGGACAGGGAGTCCAAATACCTTTTGGGATTTCATAAAGGATGGGA  
 18953 AAGTTCAGATAAGTAAGCCAAACATAGTAATAGATAATGGTTGGCTTTTAAAAATGTAATACCATACACTACTTCATTAAAAAATAGGAG  
 19045 CTGAAGAAATATGAAAATTTTACATGAAATTCATTTATCAACAAATATTTTCAAATACCCACTATGTGCAAGTCACTGTAGAGTCCATA  
 19137 GAGACTAAGGATGTGTAGCACTGCACAAAATGGGAGCACTGAGGAGGTTTCATTCCTGCAGGGACACACAGTGAATCAGATGAGTATGTA  
 19229 AAGCAGGTAATGAGTCAGAAGGAAAAATAAGCTTGCAGAAAGTGAAGCAGGGAAGGTGGACGGTAATGGGATTTTCATGGGGGGGGCTTTC  
 19321 ATGAGGAGGGGGCAAGCTATTTAAATAGCTTGGTTCATAATGCCAATGAGATATCACTCACCACAAAGAGAGAGTAATTATTTTAAAGCAG  
 19413 TTCTAATCTTTTAAAGTATGTCTGTTTATCCTTTTTCATTTTTCAGAACACAAAGTCAGGCGTTTGTCTTTGAGCTCAAGATGCAGGACA  
 19505 AAAGTAGTTATCTCTTGGCAGCAGACAGTGAAGTGGAAATGGAAGAATGGATCACAATCTAAATAAGATCCTCCAGCTCAACTTTGAAGCT  
 19597 GCAATGCAAGAAAAGCGAAATGGCGACTCTCACGAAGTAGATAGGCTTGGCTTCCCCCAGGCACATACACACTCTGTGGGTGCTTTATTT  
 19689 TTGCCAGGTGGGTATAAGAAGGAGACCTGTGTTACACAAGTACATGAGAGGTGGGACGGATAGGAGCTCTTTACAAATATCCTGTGAGCAAA  
 19781 GGTTTTGTACATTATAACTTACTTCCCTGACATTTTCGTATATGGAAATCATGTAATGGGAAGAACCAAGCTTTGGAGGCAGAAAGGGAGA  
 19873 CCTGGGTTTGTAGTGCCATAAATACTGTATTTTCAGCTGTGTAGCCCTGGGTAAACAACCTTATGTTTCTGAGCCTCAGTTGACTCACCTATAA  
 19965 AATGGGAATAAATGAAAATTTGTCTGGGAAGATGGGAAGTGTAAATAAGAAAATGAATCTCAAGTATCTGGCATAGAAATTTTACTGTATTAT  
 20057 AAAATATTAGTAATAATTAGAATGCATGGGAGCCTCAGATTAAATTTGGTGAGAAAAATCTGGCTATGTTCTTGACAATTCATGTTTACTTTC  
 20149 AACCCTTAGGTGATTCCCAACCCTGGCTTCCCTTAGAAGTACCTGGGAGCTTTTAAAAATACCATTTACCTGGTCCACAAAGAGATTCTG  
 20241 ATTTAGTTGGTCTGGGGTGGAGCCTGGGCAGGTCTGACTTTTAGGGGGTCTCATGGACGTGTCCATGTGGGCTGTTGTTTCATAGCTAGTGTCT  
 20333 AGTTCTAATTGGACGGTGTCCATGCTATACCAGCTGCTCAGTGTTTTGTACTTTTCATCACTGAGCCTGTGGATCAGTATTTTCAAAGCACC  
 20425 CCAAGTGTTCAGGAGCATCCAGAGTGGGGAACCACTGTGTTTCATTTGAAGGCACCTAAGAGAAACGGCCTTCCCTCCTGTTTCAAAT  
 20517 GAAATGCTATGAATTACAAGTATTCCGATAATCTGTTTGGCCATTTTAGATGATGAACAAAGCAAATTTGAAGGTCTGGTTCGGGTTTAG  
 20609 ATAGCTACCTGCCGGAACCTTGCCAAGGTAAACATCGTCTTATATCTTCTGCTCTTCGTGTAATGCTGTTGAAGTATGCTCATTTCAGTGGTT  
 20701 TGTCAGAAATGGAATCTGTTGAAATCATAAAAATTACATTGTGATTACCTCTCTCTTTTCTGACCTGATTACGAGGTGACGTGACTCATG  
 20793 CAGTATGATTTTCAGGTCTGTCTTCTAAAAAGTACCTTACAAAGCATTCTCCTTTTATTATTATTTAAGTGTTTTTTCCCTGATAATGCTT  
 20885 AACACTGCATCACAGGTAAGTGAAGAAATACTGAAATATGCAGGCAGATGTTCTCATAATAGCATCGTACTTCTATGTTGATACATGTGCT  
 20977 CTCCCTTACTCAGGGTAATAGACACGGTTCCAAAGGGAAGGACCTGGTAATCTTGCCACGAAACCCGGGGGTGCTGAGTTACAGAAATT  
 21069 GTTTCGGGTCACTCTTACTGGAAAAAATAAGCTATTCTGTGCTTACAAATTTGAGAAATTTAAAGTTACTGAAAGCACAAGAAAA  
 21161 GCAATCAACCATACTGCTACTTCCAGATTAAATATCTATTATGATGTTGCCTTTTAGCTTCCATATTCTTAAAGATATAAAACATCGG  
 21253 TTATAGTTGAAGTCTTTTTTAAACACTGTCTTATTCCTTCTTCTTCTCCACAACCCCAATCAGAAACAAGCACTATTAAAGTTTTT  
 21345 ACTTTTCATTTTATATCTTTTACAAATAAATCTATCATAATGATATATACAGTATGATTTAGTATGTTTAAAAATGTTTATAAATGCTAACA  
 21437 TACCATATGTATTCTGCACTTTAAAAATTTTAAATTTACCCCTTTTATTTGTACTATATAGACTTTTATTTTACTGTTCTATTATTTT  
 21529 CATTTTTTCTATTATAACAAAGCTACAATGACTGTCTTGTACTTGTGCTTGTGTATCTGAATGATTCTTTCTTAAATGAGAGAAA  
 21621 TATCTTTGTCTTCTTAGCCCTTTGCACTCTTACTCTGTTACTGCCCTTCTATTCTTTTTGATACTAGAGTGAATGGCGACCCCTCCACAC  
 21713 CCACATCTTAAACACTATAATAGAAACATGGTTTATCTATATAGGATTATAAATAGACCAGCATTTCAGCATTGACCTTTATTTTAAAGACAAC  
 21805 ATGGCTGTTCTCAAGTGTAATAATCTCCCTCCCTGGCTAGGGCTTTAGAGCATTGTTTTCTTTAGGACTTGACTGCTACCACAGTATCTTTT  
 21897 TAGCACCTGCCTATTAAAGCTAATTTTAGTGCCACCATTGTAAACCACCTCCTAGTCTGGGAAGAGTTTGGCTTGTGTGTTGTGTTATGA  
 21989 ATGTCTGTGTATCATATTTTGCATTGAGATTGCTTTTTTGTCTGGATGTTTGGGGGTTTCATAATTTCTCAAAACAAAATATTGTGCCC  
 22081 ATTTGGGTTTTAGTTTGTGTCAGCAGGTAATATATGTGATGCCATCTAGAATTCAGAAAGTAACCTTCTGCATTACTGGGTGAACGGAATG  
 22173 GATACCTAGGAGAAGATTTCATGTTATTTGAGCCTAATGTTGATTAAATTAATAATCTATGCTTTTTCTATGAGGATATACAGGAACGGTCCC  
 22265 CTCCTTCTCTTACTACCCAGCCAATATAATTCAGTATTGTTTGTATCCCAAGACCTAGGGAGATTTTTTAAAGATATACATATATTAAATATAA  
 22357 ATGTATACATTTATGTATATATACTTTTTTATAAGTATAATTGTATATTTTGTCAATTTAAATATTTGGAACATTTTTTAACTATGGGTTA  
 22449 CAAGTTAGGTTAAGCCATTTTAGTTGGTGAATCAGTTTGATTTCACCCCTGCTTCTTTTGTGTTTGTCTATTAGTTTTTATCTTTT  
 22541 TTATTGAGGTATAATTTGCAATAGCAGAATGCTCAAAACATGAATTGTAGAGTCACTGGAGTTCGCATTTGTACACTGATATAAGCAGCCCT  
 22633 CAGGCTAGCTTGTACCTGAGACCCCTTTTATTTTGTACCTCCATCACCCTAGATTAGTTTTGACTTTTCTAGACCTTCTGTGAATGGACTTA  
 22725 TACATGTAATCTTTGTGTGAGGCTTATTTAGCTAAACATGTGATTCACCTTTAAGAAGTTTTTTTAGGTCGGGCATAGTGGCTCATGCCTGT  
 22817 AATCCAGCACTTTGGGAGGCTGAGGTGAGCGGATCTTTTGTAGGTTAGGAGTTCAAGACCAGCCTTGCCAACATGGTATAAAACCTGTCTC  
 22909 TACTAGAAATACAAAAATTAGCTAGGCGTGGTGGCAGGTGCTGTAATCCAGCTACTTGGGAGGCTGAGGCAGGAGAAATCATTTGAACCTG

FIG. 12B  
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23001 GAAGGCAGAGATTGCAGTGAGCTGAGATCATGCCACTGCACTCTAGCCTGGGTGACAGAGCAAGACTGTGTCTCAAAAAAAAAAAAAAGGGTC  
 23093 CGTTTTAATGAAATAAAATGGAATGGAGAATATGAAAGTACACTGCCCTTAATAATGACATTATTTTTTATATAAAATACTGTCATTATTAT  
 23185 TTTGGTGGCACCTGCCACCATGCCTAGCTAATTTTTGTATTCTAGTAGAGACAGGGTTTTATACCATGTTGGCGAGGCTGGTCTTGAAGTC  
 23277 CTAACCTCAAAGATCCACCCACCTCAGCCTCCCAAAGTGTGAGATTACAGGCATGAGCCACTACGCCCACCTGAAAAAAACATTTTTAA  
 23369 AGTGAATTACATAAATTTTTACATAAAATAATGTCATTATTAAGGGCAATGTACTATTTATACATATAGTGTGTATGTGTCTTGCATAGT  
 23461 GATATAAAAGATATTTGTTTTCTTAGTGTGCTATTATGTATATTTATTACTTTCATTGGTATATAATGTACCTATTTTGGGAGTTCATGT  
 23553 GATACTTTGATATCTGTATACAATGTGTGATGATCAAATCAGGATAATTGGGATAGCCATCACCTCAAACATTTATCTTTGTGTTGGGAATT  
 23645 TGAAACATTTCTTACCAGGAGTCATGGTCAAACCTGAAAAATGAATCCTTGTAGAGGCTTTTACTCTTTCCCCCTGGCTTTCAGGTGTTT  
 23737 TACAAACTCTTTATTTAGGAAGGTGAAAGGTGGAAGTAATTTTTGAAGGGGAAAAGAATGAAGAAAATGGAGATGAGTTATTCACCTCA  
 23829 GCACATGGGTATCTGTGGGCTTTGCCCTTTAAAGCCCAGCTTGGTGTGAGTGTGAGCAGCCAGGCAGTAAGGGGAGACCTGTGTTCCTCAT  
 23921 CCCCAGCCTTGAGCAAAAATGCAGTTTGGCTGTTTATCATCCCCCTTCAGGGTGTCTGAACATTTTGCACCGGTTGAGAAGGCAAGAAAGT  
 24013 TGACCTGATAACTGTTGGTCATCCCATAGGAAGGATGGATTCCATGGTTACAGAATCAGAGACTGAAGTATGCAGAGGGAGGGGTGGGGAG  
 24105 AGAGAACTGTGCAAGGAGTTTACCAGGGTATGAAGAGGTAAAGAGGTGAGTATCAGGGAAGGAAGGTGCAAGAAAGGGTCAGGCTGGGAGG  
 24197 CTGGGCCACAGTTCAGTAAGATTACAAAGAAGGGCCTAGAACAATGAGGGCAGGCAGAGGTGGCTGAAGGTGTAATTTTCATGGCAGGTTCC  
 24289 TTTTCTAATCAGCTCCTCTAACCTCCTTCATCCTGTTGCCCGGGCTTTTGTTCCTACTGTGACTAAGACATAGCCAAACAGGATATGACCG  
 24381 ACAGGAAGTTGTTTCAGTGCAAAAATAACTGATGTCTCATCTGGAATATTATGGAAGGGCTCATTACTTACAGTGTGAGTGATGTAACCC  
 24473 AGGTTTTTCAGATATTTTGTATAATCTTGGAGCTTATGTTTGTACATTTAGTACTGAACATCTGTATTGTTTTCTTATTAGAGAACACACTG  
 24565 TATTTACCCTAAACAGGTTCTTTTCCCTCCTATTGTCTATTATGGAACCAACAATTTTATTGTAAATGTAACAGTGTGTAGCATCAGTCT  
 24657 TATAAATATTTTAGTTTGATACACAAACCGTAGTTCAGTTAGTTAATTGATTTCTTCCCTAGAAAAGTCAAGGAGTAACATAATCAGGTTAT  
 24749 AAACCTCATTACTAGTTATTTAATAATTTATTTCTCTGTTTACATTTATATCTTAGGTGACATCAGAACATATATGTCACCTCCTTAAAGAT  
 24841 AGTGTGAAGAAAACCCACCTTATGTTTTCTTCCACAGCTTTTCTGTTTGTGAGCTTTTATTTTTGTACTCAAAGAATAGCATCCAACCTTTTA  
 24933 CTTTGGTTTCCCCATGTGGTCTGAAAGAGAAGTAGAATTTCTCTAAATCCGGAATTGCTCACATCCTTTTACCTTTTAACTTTGTTTTAA  
 25025 GCAATGAACCTATTGTTCCAGGTAAATCTTCCACAGTTGCATGCAGGGGAAAGTATGATGTCTCAGACTTTATAGTCTCATGGAGATGGAG  
 25117 TGAGGATCAAGGGCCATGCTCAGCAGAACTTGTGAGGACCCAGCAGTTTACGGACACCTTTTCTTAATTTTAAACCAAGTCTATAATAAG  
 25209 TGCTTTCTTCCCTAGATTCCAATCCAGAAAACAATATCATTGCACTATTATACAAAGGAGCTGGCTAGGCTTGTGTCTGTGGGTGAGCTGG  
 25301 TGTTCGATTTCTGGGCTCCTTTGTGAAGAGGATGAAGTATGCTGCTGAGAAGTATAGGTGTCTTGAAGTAGTGGAAATAAATCATGATAA  
 25393 CTCTTTAAATTAAGATTATATATTTTGGCTCAAACATTTTGCAAAGTCTCCTATTCCAACCCAATCTGTTTAAATGACCCAACATTCA  
 25485 ACACATTGTTTCTGATAATTCATCCTCAGAATAAGATGCTGTTGGCCATAATCTTGTCTCTAGATTGTTTTATCTACTCGCAAATAAATTT  
 25577 AAGACACAGAGTATGCCTAAAGCTACAGCAGACTTTCTGGAACCTCTGAATGTTTGGTCCATAACTACTTCTTAAGACAAGAAGAAAAC  
 25669 CTTGTGAGGTGTGTGATAGTGTGTAATGTAGGGTTTACAGGATGGGGTGGGGTGGGGGAATCGCCCTTGGTTTAGATGAATCATTCTTT  
 25761 TCCTTGTCTCTCAGCAAACACAGTTTCTACAGAGAACAGCTCTGCCATTGTGCATTTTCTGTCTCCATTTTCTCTCATCTCTCTCCA  
 25853 CGAAACCCAGAGTAGTCAGTGGGCTTTGGGCAGGAAAGTGGCAACAGGGTGTCTGGGAAAAGCCAGTTGGCTCTTCTTACCATCACATAT  
 25945 AGACTGACCACAGGTTATTTTAAAGAGCAGAGCTGGTTTCCATCACTCTGAGAAGTGTCAACTACAGACTTTGGGATGATATTTGTTATAGC  
 26037 TGTATTTTCTCCACTCTTAGATTGTGAAGTACATATTACAAGTATTTATTTTATTATCTTTACTAAATTTTAAATAAAAAGAAGCGTGCT  
 26129 TGCCGCAATAAGTAAAAATACCCAAGTTGTTTAAAGAAAAGTTACCTTTTCCCTTCATCCTCCATCCCACATTCTTGAGAACCTGAAG  
 26221 TTAATAACCGGTTGCAATTTCCCTTTTACCAAACGATTGCTCATAGAAATATAGATAAACATATGTAAGGTTTTTAAAGTTTTTAAATAA  
 26313 AATATGTTTCATGATATATACATTATTCTGAAATTTCTGTATCACTTAAAAATATTTTATAGATGTCCCTCTGGGCCAGTGGAGATCTGGT  
 26405 TCCCCCTTACATACATATCAGCAAGCTGCATGATATTTCAACTATTGTACTGCACAGTTTATTGAGCCATCTCCCTATTAATGAACATTTA  
 26497 AGGTTTTTTTTTTCAGTTTTTAGCCTCTACAAACAGTACACAATAAACATGACATTAAATACTTGTGCTCTTATTTTTCAGTAGGAGAAAT  
 26589 CCCCATGTGGAATTTTAAAGTCAAAGTTTATTGTGTTTTTAAATGCTTTAAACATGCCAGGTTACCGTCCCAAAGGCTATAACAATTCAC  
 26681 ATTTCTGTTTCTCTGCATCTTACCAGACGAGTGTAAAATGGTATTTTACTGTGCTTTTCAATTTATATTTTGTGCTTATTAGTGATATTTT  
 26773 CATATTTTCATATATTTATTTGCCATTTGTGTTTTTCTTCTGACTTGCTTGTTCATTTGTTTACCTTGTGTTTCTTCTGTCTTGTGTAGT  
 26865 GTAATAGTTTAGACTCTGAAGCCAGGCAACCTGAGTTAGAAGCCAGGCTCTATTTTCATGATGAGGTCTTTGGGCAAAGTACCTAACATTC  
 26957 ATGCCTTAGTGTCTTCTCTTTAATGAGCAGGGATAATAATAGTACCTGCCTCCTAAGGTTGTATAAAATTAATGGGCACTTAGGGTAAT  
 27049 ATCTAGCAGGTAGATATTGGCTATTATCAATAGTAGCTCTTATCGTTACTATTCTTCCAGATACTGTTTCTGACTCTGGGCAAAGTCTCTG  
 27141 CTACCCCTGAACCACATTTTCTACCTCTTAGATTTTACTTGGTAATCCATCAGCCACTGTTGGGCATCCTCTGTGTTAATGCATCATCT  
 27233 TAGACCTTAGGAGGGATGGGAGGAACTTAAGAAGCCGAATTTGCTTTTTATTTATCTTGTAGCAGAGCAATAGATGTATATTAGGTAGATT  
 27325 ACAAGCTTTTAGGTTATTTTGCATCTAAAGCTGTCCCTCTTTTCCAATAAATGATGTCTGTGGTAAAGAATATATCTGTTGGGTGTTAGT  
 27417 GACAAAATCAGAAATGCTTTGTGTCTATTTGGCTAGTAGTTAATGTTTTCTTTTATTTGTGTCTGCATTCTTATTTGTTCTTTAATTATAC  
 27509 CGAGCTCATTAGCAGTTATCTTGCTTTATTCATTTCTTATCTCTAGCATAGTCAGCTCAAGACAACAAGCATCTTTCAGAAAGCCACTAG

FIG. 12B  
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27601 GAATTGCATCTACATTAAGAACCCTCCTCTGCTCTAGCGTCTGAGAACATAACACAGTATTTGCCTTTGTTGAAGGGCTCAAGCGGACGA  
 27693 TTCAGAAGTAGAATAGATAACTGTTGGTGGTGGCTTGACGACCTAGTACTGATGGTTTTGTTAGGAAACACCACAGGCAGTATACAATGTA  
 27785 AAGCAAGTTCTTTGGGTTCAGTTAAATAGATTCCACTTGCACGTGTTCTCACTCTTTGGTGTGAAAAATTAGGAAAGGTGATAGGCAGGAT  
 27877 AGAATAAAATGAAGTGGTCCCATCTCCCATATGGAGAGCGCCTGCCTCCACCACAGACACATGTTTTGCCCTGGAAGCATAAACAGAAGATT  
 27969 GCAGGAACGCCCCCTCACCTCCATAGCCTTCAGGCTCCCATCGATAGCATCAAGATAAACTTGGTGTGGCAACAGACTTGGGCCATCATCTT  
 28061 GTTTAACATTTTTTACCTGGAAGTGAAATGGAATCCAGAGAGGCTAAGTAGCTTGCACAGCTACTTAATTGAACTAGAACCAGAACCAGTT  
 28153 TCTTAGTATTCTGGTGCCTATTTTATATAAACATAGACAGCTGATCATGGTAGTTGGATCATTGCTAAAGACCTATTATATACAACAATCG  
 28245 TATGGCTAAGAAGATTAGATGCTTATTTCTCGTTATCCATGATTAGAAATGTAATAAGAGACTTTGTTCTGTACCAACAGAAGAGACAA  
 28337 GACGCCTTTTCTGCTGTGGTTGTGAGTGCCCATCAAGTGCTGAGATGTGACTCATGTCTTTGGGAAAGTAGCAGATGAGAGAGTACATT  
 28429 TATTCGACTCCATAGACTTAAGTGTGGAGACTGAGAGTAGTGAGAGCTCAGACTGACAAGAAGACAGAATATAGACTTAGAGGCACCAG  
 28521 GCATGAAAAATCATAAAGATGGAGATGACTTCTATCTGTGTAATGTCTGAAAAGCCTCTCTCTTTCTGTTCCCAATCCTTCATCTCCAG  
 28613 CCTCATCTCTGCCACCATCTGTGCGTTTTCTTCCGTGGCCTCTCTTCTGTCCACCTCTTCAATGTTGGGCCCCAGGATTTTGTCTTCAGA  
 28705 CTCACTTTCACCTCTCCCTCAGGACATCTCATCCACTCCCAAGGCTGGAAGTCCAGCCTTCCTCTCAGCCTTGGCCTTAAGTTTCATCCCT  
 28797 TTAGCTGTCTATTGGATGTTTCCAGTTGGAAATCCACAGGCATCTCTACCCAGGCGTCTTACACAAGATGATAAAATATTATCATCTT  
 28889 TTTGGCAGATTTGTTTTCTCTGAGTTTCTGTGCTGTTCATGGATTCAACATTGAGCAGGCTGCCCAAGCTAGAAATGTGGATTGTAAAT  
 28981 CGGCCCTGCTGTGAGACTGGGAGGCTGGTGTGATAACCAAGAAGACATTGTGGGCTCTGGGTCTTATCCTTTTTAACCATTGCCTCAG  
 29073 CCTGCCCGAGTGATGCTTCTGAAATGTGGAAGTCAATTTATCTCTTACCTAAAAGGTTGCAGGATATTTAGATTCTGAATGAAATCCCC  
 29165 AATCCTTTTTTTTTTTTTTAAAGTAAAGCAAGTTTATTAAGAAAGTAAAGAAATAAAGAATGGCTATGCCATTGGCAAAGCAGCCCTGTGG  
 29257 GCTGCTGGTTGCCCATTTTTATGTTTTTCTTGATGATATGCTAAACAAGGGGTGGGAAATCCCAATCCTTGGCATTCAAATCCAGACT  
 29349 CATTTCTTTTCACTTTTTTTTTTAAATCATGCCCTGCCCTTCAGTTATGATGAGTGAAGTGGTCAITGCTCAGGTGTGACTTGTCCCTTTC  
 29441 ACCTGCTGTGCTTCTCCTAGAAATGCGCTTTTCTCCTTCTGGCCAAGTGTCTTGTCTTCCAAATGGGCTTCCCTTGGGAGGTGGTTT  
 29533 CTGACGACCACCCCTAGTCCAAGTCAGCTCCCACTGTACTTTAACTTTCTCTGTCTTCTTATTACCTGTTGATATGCTCTCTCCCCAC  
 29625 CTGGTGTCTTGGGACTAGGGACTTCCTTCATTACATTTACATAACTTGAGGCTGGCTCATAAGAGGTGCTTAATGAATATTTATTG  
 29717 AATTAATTAGCATCTTGTCTTCAAGATCAGCCATCATTTTCTCTATCTCATCTTCAAATATATTCTTCTCTTCCCTTCTTGCACCC  
 29809 AGTCACAGACTGGACTCTATTAAATCCTGTCTATCATCTGGGCTCATTTCCATCCTCAGTGTCTGTCTGTGCATCCTTTTCATTGAGCCAGG  
 29901 GATGTTGAGCTCGATTCTGCCCTTCATTCCAAGCCTGTCCCATATTCCATTACTTTATGAAGCCTTTCTTGACACACAGATGCTTAATTAT  
 29993 TCTCTTTTGCTTTCTTTGTGTGACTTTGACTCTGCCACTGGTTGTGAGCTTCAGAAGGGCAGGGATCTCACCTTCACTTCTTTTTCTCCT  
 30085 AGTGCTTTCTTTGTGTGCTGCACACTCCCTGGCACACACAGCGGCTCTCCAACACGAGGCAGAGCTTTCCAGCAGCCTCAACCTTCAGGACT  
 30177 GGGCAGCTTTTAAATGTATTGGGCACCTTTGCAAGAAAAGGATTGTGTTAAATGTAATTTTCATGTATCTTGTATCAGAGTGCAAGAGAA  
 30269 GCAGAAATCAAAGTGAAGAGTGAAGCAGAGTCAAACCTTTTTATTGGACCCAGATGCCAGGTAAAGAACTATCTAAATGTTTAAATATTA  
 30361 AAACCAAATGTGGGAGAGAAAATCATCGATGGGCTTATTGTTTATTGTTGCTTTGTTTATTGTTGAAAAACAAGCAAAATAACTATAGA  
 30453 AAATTTGGGAAAAAGAGGAAAAATAAAATGTATAATCTATCACCATAGCATTACTATTGTGAATATTGATATTCAATAGATGTTTGAAA  
 30545 ATTGGGAGAGATTATTGAAAAGACATTCTCAAGTTCACAAAGAACATCTAATTTACCTGTAAATAAACCATCAGAAAAACAAGGTATCAC  
 30637 TGCAGTTGCCTGGGAGTCAGTGATAATCCCGACTAGCCAGGCTCAGGCTCAAATACAAACCTTTTCCATTAACTCTAACGATAAGTACT  
 30729 TTTCTGTTTCTCACAACCTCATAACCATACGATGTGTGTTTATATGTCTATATTTTTTATTGCTTTTAAAGAGTTTTGTTTATCATT  
 30821 GTAAATATACATAATATAAAATTTACCATTTAACCATTTTTAAGTGTACGGTTCAGTGGCATTAAATACATTCTCATTGTTGTACAACCA  
 30913 TTACCACCATCCATTTCAGAACTTCTTCATTTCCACACGGAAGCTTTGTATCAAATGATAACCTTCTTCTCTTCCCCCATCCCT  
 31005 AGTAACCTCTGTCTACTCTGTGAACCTGCCTATTTTAGGAACCTCATAAATGTGAATCATAAGTATTTGTCCTTTGTTTCTGGCTTCTT  
 31097 AAACCTAACATGTTTTCAAGGTCAATCCATGTTGTAGCATGTGTCAGAAATTCCTTCTTCTGTGGCTGAATATTCCATTGTATGTATATA  
 31189 CTACATTTTATATATCCTTGTAATCTGTTGATGGACACTTGGTTGGATACTTGATGGACATTGGTTTGTGTTTATGATCATAATTTTCA  
 31281 AGCTCTGTATTTTTTTCAGTTTCATCCATTGAGTAGGTATACCATCATGTCTTTTTTTTTTTTGTCTTTTTTTTTTTTTTTTTTTTGGGCAGAG  
 31373 TCTTGCTCTGTGCCCAGGCTGGAGTGCAGTGGTGAATCTCGGCTCACTGCAAGCTCCGCCCTCGGGTTCACACCATTCTCTGCCTCAG  
 31465 CCTCAGCCTCCCAGTAGCTGGGACCACAGGTGCCACTACCACACCTGGCTAAATTTTTTGTATTTTTTGTAGAGACGGGGTCTCACTGGG  
 31557 TTAGCCAGGATGGTCTCGATCTCTGACCTGGTGAAGCCGACGCTCGGCTCCCAAAGTGTGGAATTACAGGCGTGAGCCACCGTGCCG  
 31649 GCCCATGTCTTTGACCATGTTTATAAACTATGTGTGAAGTACTATAAACCATAGAAACCGATTATATAATAGCAACACTATTGTGAGTAAA  
 31741 TAAGTGTATATAGCTTTTCCATATTTATTCGTTTCTTTGGATGCATTATGATGTTTTTTTAAATAAGAGCATAACTTATTTATATGT  
 31833 TTACATTTCTTTTAAAGAAGCTTGACTTCTCATCAGCTGAGCCAGAAGTGAAGTCATTGGAAGAGAAGTTTGGAAAAAGGATCCTTGTCAA  
 31925 GTGCAATGATTTATCTTTCAATTTGCAATGCTGTGTGCCGAAAATGAAGAAGGACCCACTACAAATGTAATTTTCATTTTAAAAATAAAC  
 32017 ATTAATAAAAAAATAGGCAGAGTTTCAGATGTACCTTTACAGTGCAGCCTGGATAAGAAATCCTAGTCCCTGGTATCAAAGAGGTGCAGTG  
 32109 TTTGGATCAGGATATGGAGGTTGTAGCCTGCAAGGACAGGATGTTCTGTATGGAAGATGAGGGTGGCAGGTTTGTGCTCAGCTTTCCAGGA

FIG. 12B  
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36801 ATACCTTTTAAATCGATATAGATAGGTGCATGGATGGGTCAATAGGCCTATTCTGTTTGTGTTTCAGAGACAAAGAGGATTGAATGTGTAA  
 36893 AACTGAGAAATACATAAGCCAGATTTTGAATAATCATTGGTAGAGTCACAGAGAGGATAGACACTGCTCGGAGAAGTGCTACCTGGAAC  
 36985 TGGCAGGGTGCACGGTAGTGTAGCTGCAGAGCTGGGATTCAAGGACCAACCACATGCCTCCAGCTGGAAGTCAGGGCAATCCAGTGAGGC  
 37077 CTGGGGTGATCTTTATCTCTTGAATCTACTTGTGTTAAGCATTGACTTGTGTATATTGTTTCTTAAGCACAGCCATTGGCTGGAACGTGTTT  
 37169 CTATGTAAATTGATTTAGTTGTCTCATCCCATAGATGTTTCCATGTTTTTAGATAATGAGATTTCTGTTGGCTATAGCCAATGGAATAA  
 37261 TAATTAGACTTCTCATAGAACTAGACTTAAATAATGAATTGATTTTGGTGTGTTTGGAAACCCAGTTTAGAAATGTGCTTTGCCATTTCAG  
 37353 GACATTGTTTAAGGATGCATCTGGAAATCTTGACAAAAATGCCAGATTTTCTGCCATCTACAGGCAAGACAGCAATAAGCTATCCAATGATG  
 37445 ACATGCTCAAGTTACTTCGAGACTTTCGGAAGTGAGTTTCAAGGTCTTATTTCCACACCTGAAAAATAGAAGCTGTGTAGTGGGGAGGGAGG  
 37537 AACAGGGGAGCAGTCACTTAGGTTGCTCGATTAGACATCAGAGGGGATGGCAAATGAGCGTGAAGCATTTCTCTCAAAACCTTGAGAAGAAA  
 37629 GATGGGGTGAAAAATCAGAAGAATAACCAGTTAATTGAAATCTGTAGAGGATGTTTTGGGTGGTGTGTGAAGGGTGGACTGGGTAAGGATG  
 37721 AGCCTATGGTGGGGAGGAAACAGTTGAGGAACCTTGTCAAGAGGTGAGAAAGGACTCAGCAAAGCCACTGCAAGTGCAACAGGAAGAAGGG  
 37813 GACAAATTCAAGTCGTGCCAAAGAGATACGATGACTGGGTCTTGGCTTGGGGTGGTAATAGTCTAAGATAAATAACTTGCAAGGTTTCTAAC  
 37905 TTGGAAGTTTCTGGCACCAGTTGTTGCTTAGCTTGTGGCAGCATTGCTCCACTCTGCCCTCTGGCCTCACATGGTCTCTTCTGTGTGTCTC  
 37997 TGTCTAAATTCCTTCTTAGAACACTAGTGATAAAGCATCAGGGCAAGCCTAGTGACCTCATCTTAAGTATTGATCTGCAGAGACCTTG  
 38089 TTTCCAAATAGGTCACATTTATAGGTACAAAGGGTTGGGACTTCACCATGCTTTTGGAGGACACAATTCAACCCATAACAATGAGGCAAGA  
 38181 GGGAGCAAGGAATGTGTCAACATCACAGGGCCGGCAGCTTCCCCAAGTCAGTCTCACCCGAGGGTCTGTGTTCTTAACCTCTATGCTGTTT  
 38273 TGCTGTACATCTTAAAGAGTTCACTCTGAACCTTTGAACTGATTTCTTTGCTAGGGAGATGGGTCTTAGAATTTTCTGGGAAATTCT  
 38365 GGGAAATGTGAAAGAGCTGAGGGCGCTAGAAGATGTGAAGTGAAGAATAGCTGAGAGCCAAATGCTAACTATTCTATGCCAAAGGTATCCT  
 38457 TGTTTTTTTTTTTTTTTGTGCATATCAAAATAGCAATCTTATCAGTTTGTCTAGAATCAAGAATGATTGCTTAGCTTTCTTTAACCTTATT  
 38549 TTACCTTTTTCTTATCTGTCTTCAAGTAGTAGGAATAGAAACGATATGAGTCATAGAAGCAGGCTCAATAAGTTCTGAAACACAGAGACGTG  
 38641 TTCTTAATCAGAATCCAATCACGTCCATGTCAGCAGGGCGCTTCAGCCTTCACAGCGACGTGAAATCCCTTGTCAAGAGGCTCAAAAAGGTA  
 38733 GAAAGGATTCTCAAGGTCCTTTTCAAGTTATGTGATTATACAGTTTGTGACTGCTTGTATGTTTCCCTGTTTGGAGCTTTAATGAGAAGTGC  
 38825 AACCTCAGTTTGTCTAACATGCAGCTAAGGTTGGCCTGTTTCAAGCAGTGTGCATGCCCGCTGGGTGATTGGAATGAACCTTTCACA  
 38917 GCTCAGTAGGGAATTGAGAAGGGGAGAGGAGATACTGGTGAAGGATGAGGCCCTGCTGGGTAGCTTCCAGGGTCTCTGGACCATATA  
 39009 GGTGCCCCAAATTCAGTCACTATCTGACAGTTTATGACCTGGTAAGGACACAGGCTTGGCCAGGGAGTGCCCTGGATCCCTATGAAT  
 39101 CTGTTATTATGAAAGACTAAATAAAGAATAGTACCCTATTTTACTTTTAAATCATAGAGTTCTTTAGTTTACAAACATAATACATGTT  
 39193 CATTTTAGAAATTTTGAAGAAATACAGAATAAAGGATGAAAAAGGTTTACTACTAGTTTAACTTCGTTGGTGAACCTTTGGAGAACT  
 39285 TTTTTTTTTTTTTTGGAGATGGAGTCTCACTCTGTCCCTCAGGCTGGCGTACAGTAGCAGGATTCAGCTCACTGCAACCTCCGCCCTCCGAG  
 39377 TTCAAGCGATTCTCTGCCTCAGCCTCCCAAGTAGCTGGGACTATAGGCGCCACCCTACGCTGGCTAATTTTTGTATTTTAGTAGAGA  
 39469 TGGGGTTTACCATATTGGCCAGGCTGATCTCAAACCTGCTGACCTTGTGATCTGCCCGCTCAGCCTCCCAAAGTGCTGGGATTACAGGCAT  
 39561 GAGCCACCGTGGCCAGCCTAGGGGGGAACATTTTTTTTTTACGTTTATTCTTTTACATTTTATTTTAGTTTATCTTATGTAGCTATGATCAT  
 39653 ACTAAATATGTAATATTTCCCTGCACAACCTCAAGTATTTCTGAAAGTGTTATATATACATTTTATAGACATCATTTTAAATGCATAATA  
 39745 TTATAATAGTCCATTGAGATAGACCATAGATTATTTAACTCTTCCCCCATTTTTTGGACTTTTTTTTTTTTTTCCGAGATGGAGTCTCGCTCT  
 39837 GTCGCCAGGCTGGAGTGCAGTGGCACCATCTCAGCTCACTGCAACCTCCGCCCTCCAGGTTCAAGCAATCTCTGCCTCAGCCTCTGAGT  
 39929 AGCTGGGACTCCTGAGTAGCTGAGTAGCGCATGCTGCCAGCCCCGCTAATTTTTTTTTTTTTTTTTTTTTTTTGTATTTTAGTAGAGA  
 40021 TACTAAATATCTCACCATCTTGCCAGGCTGGTCTCAAACCTCTGACCTCAGGCAATCTGCCCGCTCAGCTTCCCAAAGTGCTGGGATTAC  
 40113 AGGTGTGAGCCACCATGCCAGCCATTTTTGACTTTTAAATGTGTTTCTGATTTTTCAGAATATACCTATAAGCCACAGTTAGAATCTTTA  
 40205 AAAAAATCTCTCTATTGGTAGTGGGTAATATATATCATACATACTATATATCATATAGTAATTATGTCAATTTTTTGGATTTCAGAAA  
 40297 ATTTCAATCTTACTAATTTTTTCAAAAACAGTCACTTTAGTTGGATAGATTTCAATATTTTCTTCTCGCTCAACTACCATGCAACTCTTAA  
 40389 TAACCATGAGGTGGGTCTGCGTGTACTTAGGAAAGTGAATACACTATATTATTAAGGAAGAAAAATATATCTGTATTACTATATTTTTGA  
 40481 AAGAAAAATATATATTCTTTTTGTATGTAATGAAGAAATGGATAAGCAAGTAGCTATCTAGATGGAAGATAGGCATAAAAAATAGCTATTTA  
 40573 GGATATATGCCAAATAATCATGGTTATCTCTGAGGGATGGGTTGATGGGTGATATTTACCTTCCACTTTATAACATTCTGTCAATTTTTATA  
 40665 TGAACCTTTTAAAAAATAACACTTTTATATTACAGACAAAAACAATGAAGTTTTTATATGTGATGGAGGTGGAGCCCTGTCTCAGAAG  
 40757 TTACTTCTTAGGCTGGTTAGCTTGAGACTTCCCCACAGTGGCGGCTCCTCAGGGGACGCCCAGTGATGGTCTGTCTTCACTGGAGGCTG  
 40849 GGGAGTGGGGCTTCACATGGTCACTAATTTGAAAGTGATGGGAGCAGAAAGCCTGTGGCCAGGCAGAAAGGAGCCAGGGAAAAACCAAGTGT  
 40941 GAGTTCTCTTCTGCACACCATTCTTCATGCATGTGCTCAGCAGGAGGGCATTGGTGTGAAGGGTGTGCTCCAGGTGGCCAGTTAGAGACCC  
 41033 AGAAACCTGAAACAGGGATCCGATGGTGACAGCATAGAAGACACAGCAGGATAAGTGAGGCCACGCTCCTCAATAAGTATTCAAGAAACT  
 41125 TTGGTGCCCACTCCCGTATTCTTCAACAGAGTTAGGGGACGTGGAGGATTCTTTTTTCAATTTTTTAAAAATCTTTGCATTGCTATTTTT  
 41217 CTTTCTCTGTATATTTTACAGGAAATAATCTCATGTGAGTGGCTGGGCACCGCTTGGATCCAAAGCTATGTTTCTACCCCATGATTG  
 41309 TCTCAAAATGTTATTTAATAATGCATGAAAAAATTTCTTACGCTGTCTCAGTCTTAACAAAACAGCTGCCAAAGCTCATAAGCCACTTTC

FIG. 12B  
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41401 CTTTTTCCCTTGCAATAATTACCCAGGGATATGTTCCAAGATTAGTAAGAAAGCGATTCTGTCCGATAGATGATAATTGCTAACATTTTATA  
 41493 AGAAGAGAGACTTGGTACTTTGTATTGTATTGTTTCATGGTGGTATCTCATGGATAAGATGGTATCTCATCTTTTCCAACCTCTGCAGGAAA  
 41585 TCGAAGACATGAAGGCAAAGTATAAAAAATAGAACGTTTTCTTTAAAACGTAGACCTTTTTAATGGTACTACGTTGGATAGTTTAGGTAATA  
 41677 ATACTACTAAAGTTTTTGGGTATGCAGCTTAATGTGTCTGTGTTTATTGTACACTCATCTTCTTTGCATCCAGGTTTACAGTCTTACCCC  
 41769 GATTTTCGCTCTGGTTACACTGCACTCAAGCCAAGTAGGGCTGCTTGACTTTCTCTAAACCCACTGGGGACTTCCCTCTGCCATGCTTTTCTC  
 41861 TCTGCCCAAATTGTGTCCCTTCCCTGCCTCATCAAGCAGCACATAAATCACAAACACATGCAGCATAACACTTCCCTTTTCTTTGTCTT  
 41953 TCTCAGGGAACCTACTCATCTTTCAAAGCCCACTGTGTGGCTCACTTCTGTGCTGGGAGTCTTGGAGGCGGTACTTGGCTTCTGTGCCTG  
 42045 AGCCGCTCTCTTTTTAAGGGTGGATAATAACAGCCCCCTGCCCCCTAAAACCGTGGTGGGAATAAATGCAAAGGCATTAAGGTGATTTCT  
 42137 TCCCACCATGAATACTGATCTCATCCCGTGTTCCTCTCGATAGATCTAGATACTCTGCCTTCTGGTAGAGGTTTGTACATACTCTGTGAAA  
 42229 GTGATTGCCCTCATATGCCGTAAGTAGCTTACAGTGTCTACTGGACTTTTGGCTTCTTGAGGAAAGAAATATGTCTTGTTCATTTCCTCC  
 42321 ATGGTCTGAGTACATACATTCAGCATATCCTAAGCACTTGATAAATGCTTATTGAATTTTCTTCTTAGACATAAACTCAGTGGTTTTTGT  
 42413 TGAAACAAAATATCTCAAATTTCTTTCAATCATATATAGTTGTTTTTTTTTAAGTGACACCAAAGCTTTTAGGGAATATTTCCTTTCACAA  
 42505 AACACAGTTAGAAGATTAAACTCACCACCAATAGCAGTCCAAACATACCTGTATTGCCAGCTAATCATTTTAACGAGCCAATACAGGAAGTC  
 42597 AGGAAGGGAAGACCGGCTGCAGAAACACTTAGATAAGGACCCCAAATCTGTTGGCATGGGAGGACTGCTAGTTGATGATACCATTCCCATTT  
 42689 CCTCTGTGGGAATTGTTGAGTCAGCAGAAATGGATGGGCAGTGGGAAGGGAATTTTCTAAGAGAGAGTTTGAGCCTCACTTCTACATTC  
 42781 ACACAGAGACAGGAGCAGTTCACAGAGGCCAGGCATCCTGCAAGTGTCTGTATTGCATGCTTACTTAATTCGTGTAATTTTAAGATGAGTTT  
 42873 TCATGTTCAAGGATTATTTTATAAATTTTGCATAGAATATAGGTACTCTTTAGCAAAACAAAGCAAAAAACCAAACCTATTCTCAGTCATG  
 42965 AAAGAATTCAGTTTGTGTAACACGCACACAACCACCACTTTGGAAGTGCATAAAAAGGCAGTAAATCTTTATTGCCTGTGAGTGTTTGATG  
 43057 TCTAATAAACCAGATTCAACATAAACCATAAACTTTTGAATGGGTTTGTGATTGGGTTTTTAAAAACTTAAAGCTGGCAAAAAAACA  
 43149 ACTTTTAAAGCCCATGTGCTACATAATATGGAATAAAGTAACTCAGAAATGTGCTTGGAAACACATGGAAAGAACGTCTTTACAGAAGCAGCAA  
 43241 CTAGAAGTAAATCTCTCAGCAGAGGGAGGAAATAGAATAAGAAATAACTATAGTTAGGCACAGAAGGACACAATACACTATAGGAAGATTT  
 43333 CCAGTGAAGATCATTTAATTAAATATGTTGCTTAGAAACGTATTTTAAATGTGTTCCACCTCTCTCAAAAATTTATATGTGGAGGATGTTG  
 43425 GAGTGATCTTAAAAATGGTGATGAAGATGCCTGTTCATTATAGGTGGAAATAATTAGGAGGGGTGAAATCCATTACCTTGCATACCTTAC  
 43517 TTATATTTAAAGTATAATTGTGAATAAA

FIG. 12B  
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hCLASP4 -----MFPMEDISISVIGRQRRTVQ----- 20
hCLASP5 -----MTHLNSLDVQLAQELG----- 16
hCLASP3 -----MAERRAFAQKISRTVAAEVRKQISGQYSGSPQLLKNLNIVG 41
hCLASP2 -----MLLFFPYDDFQTAILRRQGRYICS----- 23
hCLASP7 -----MAASERRAFAHKINRTVAAEVRKQVSRERSGSPHSSRRCSSSL 43
hCLASP1 MSFRGKVKREPSEFWKKRRTVRRVIQEEFHRFSSQEKPRLLEPLDYETVIEELEKTYRN 60
      ...

hCLASP4 -----STVPEDA EKRAQSLFVKECIKTYSTDWHV VNYK 53
hCLASP5 -----DFT 19
hCLASP3 N-----ISHHTTVPLTEAVDPVDLEDYLITHPLAVDSGPLRDLIEFP 83
hCLASP2 -----TVPKAE EEAQSLFVTECIKTYNSDWHLVNYK 55
hCLASP7 G-----VPLTEVVEPLDFEDVLLSRPPDAEPGPLRDLVEFP 79
hCLASP1 DPLQDLLFFPSDDFSAATVSWDIRTLYSTVPEDA EHKAE NLLVKEACKFYSSQWHV VNYK 120
      ::

hCLASP4 YEDFSGDFRMLPCKSLRPEKIPNHVFEIDEDCEKDED-----SSSLCSQKGGVIKQG 105
hCLASP5 DDDL DVVFTPKECRTLQP-SLPEEGVELDPHVR-----DCVQTYIREWLI 63
hCLASP3 PDDIEVVYSPRDCRTLVS-AVPEE-SEMDPHVR-----DCIRSYTEDWAI 126
hCLASP2 YEDYSGEFRQLPNKVVKLDKLPVHVYEVDDEVDKDED-----AASLGSQKGGITKHG 107
hCLASP7 ADDLELLLQPRECR TTEP-GIPKD-EKLD AQRV-----AAVEMYIEDWVI 122
hCLASP1 YEQYSGDIRQLPRAEYKPEKLPSHSFEIDHEDADKDED TTS HSSSKGGGGAGGTGVFKSG 180
      :: .      : * . : * .

hCLASP4 WLHKANVNSTIT--VTMKVFKRRYFYLTQLPDG SYILNSYKDEKNSKESK-GCIYLDACI 162
hCLASP5 VNRKNQGSPEIC--GFKKTGSRKDFHKT-LPKQTFESETLECSEPA AQA--GPRHLNVLC 118
hCLASP3 VIRKYHKLGTGF--NPNTLDKQKERQKG-LPKQVFESDEAPDGNSYQDDQDDLKRRSMSI 183
hCLASP2 WLYKGNMNSAIS--VTMRSFKRRFFHLIQLGDG SYNLNFYKDEKISKEPK-GSIFLDSCM 164
hCLASP7 VHRRYQYLSAAY--SPVT TDTQRERQKG-LPRQVFEQDASGDERSGPDSNDSRRGSGSP 179
hCLASP1 WLYKGNFNSTVNNTVT VRSFKKRYFQLTQLPDNSYIMNFYKDEKISKEPK-GCIFLD SCT 239
      : :      : : * : : . : .

hCLASP4 DVVQCPKMRRHAFELKMLDKYSHYLA AE TEQEME EWLITLKKIIQINTDSL VQEKKETVE 222
hCLASP5 DVSGKGPVTACDFDLRSLQPDKRL ENLLQQVSAEDFEKQNEEARTN-----RQAE 169
hCLASP3 DDTPRGSWACSI FDLKNSLPDALLPNLLDRTPNEEIDRQND DQRKSN-----RHKE 234
hCLASP2 GVVQNNKVRRFAFELKM QDKSSYLLAADSEVEME EWITILNKILQLN-----FEAAMQEK 219
hCLASP7 EDTPRSSGASSI FDLRNLAA DSSLPSLLERAAPEDVDRRNETLRRQH-----RPPA 230
hCLASP1 GVVQNNRLRKYAFELKMNDLTYFVLAAETESDMDEWIHTLNRILQISPEGPLQGRSTEL 299
      * : *      : : . : :

hCLASP4 TAQDD ETSS----QGKAENIMASLERSMHP ELMKYGRETEQLNKLSRGDGRQNLFSFDSE 278
hCLASP5 LFALYPSVD----EEDAVEIRPVPEC PK EHLG-----N-----RILVKLLTLKFEIE 212
hCLASP3 LFALHPSPD----EEEP IERLSVPDIPKEHFG-----QRLLVKCLSLKFEIE 277
hCLASP2 RNGDSHEDD----EQSKLEGSGSGLDSYLP ELAKSAREAEIK---LKSESRVKLFYLD PD 272
hCLASP7 LLTLYPAPD----EDEAVERCSRPEPPREHFG-----QRILVKCLSLKFEIE 273
hCLASP1 TDLGLDSL DNSVTCECTPEETDSS ENNLHADFAKYLTETEDTVKTTRNMERLNLFS LDPD 359
      .      :      : : : :

hCLASP4 VQR LDFS----GIEPDIKP-FEECKNKRFLVNCHDLTFN ILGQIGDNAKG PPTNVEPFFI 333
hCLASP5 IEPLFAS----IALYDVKERKKI SENFHCDLNSDQFKGFLRAHTPSVAASSQARS AVFSV 268
hCLASP3 IEPIFAS----LALYDVKEKKK ISENFYFDLNS EQMKGLLRPHVPPAAITTLARSAIFSI 333
hCLASP2 AQK LDFS----SAEPEVKS-FEEKFGKRILVKCN DLSFNLQCCVAENE EGPTT NVEPFFV 327
hCLASP7 IEPIFGI----LALYDVREKKK ISENFYFDLNSDSMKGLLRAGH THPAISTLARSAIFSV 329
hCLASP1 IDTLKLQKKDLLEPESVIKPFEEKA AKRIMIICKALNSNLQGCVTENENDPITNIEPFFV 419
      : :      : : . : . : : . : * :

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FIG. 13  
1 of 6

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hCLASP4 NLALFDVKNCKISADFHVDLNPSPVREMLWGSSTQLASDGSP---KGSSPESYIHGIAE 390
hCLASP5 TYPSSDIYLVVIEKVLQOGD----IGDCAEPTYVIKESDG-----GKSKE-KIEKLKL 317
hCLASP3 TYPQDQVFLVIKLEKVLQOGD----IGECAEPTMIFKEADA-----TKNKE-KLEKLKS 382
hCLASP2 TLSLFDIKYNRKISADFHVDLNFHFSVRQMLATTSPALMNGS-----GQSPSVLKGILHE 381
hCLASP7 TYPSPDIFLVIKLEKVLQOGD----ISECEPYMVLKEVDT-----AKNKE-KLEKLRL 378
hCLASP1 SVALYDLRDSRKISADFHVDLNFHAAVRQMLLGASVALENGNIDTITPRQSEEPHIKGLPE 479
. . *: *: :. : : : . . . :

hCLASP4 SQLRYIQQGIFSVTNPHPEIFLVARIEKVLQGNITHCAEPTIKNSDPVKTAQKVHRTAKQ 450
hCLASP5 QAESFCQR-----LGKYRMPFAWAPISLSSFFNVSTLEREVDVDSVVGRSPVGERRTLA 372
hCLASP3 QADQFCQR-----LGKYRMPFAWTAIHLMNIVSSAGSLERDSTEVEISTGERKGSWSERR 437
hCLASP2 AAMQYPKQGI FSVTCPHPDIFLVARIEKVLQGSITHCAEPTMKSSDSSKVAQKVLKNAKQ 441
hCLASP7 AAEQFCR-----LGRYRMPFAWTAVHLANIVSSAGQLDRDSD----SEGERRPAWTD RR 429
hCLASP1 EWLKFPKQAVFSVSNPHSEIVLVAKIEKVLGMGNISGAEPYIKNPDSNKYAQKILKSNRQ 539
: : : : : : :

hCLASP4 VCSRLGQYRMPFAWAARPIFKDTQGSLLDLDGRFSPLYKQDSSKLSSDILKLLSEYKKPE 510
hCLASP5 QSRRLSERALSLEENGVS NFKTS-----TLSSVSSFFKQEGDRLSDEDLFKFLADYKRSS 427
hCLASP3 NSSIVGRRSLERTTSGDDACNLTSFR-PATLITVTNFFKQEGDRLSDEDLFKFLADMRPS 496
hCLASP2 ACQRLGQYRMPFAWAARTLFK DASGNLDKNARFSAIYRQDSNKLSNDDMLKLLADFRKPE 501
hCLASP7 ---RRGPQ--DRASSGDDACSFSGFR-PATLITVTNFFKQEAERLSDEDLFKFLADMRPS 483
hCLASP1 FCSKLKGYRRFAFAWAVRSVFKDNQGNVDRDSRFSPLFRQESSKISTEDLVKLVS DYRRAD 599
. . : : * : : : * : * : : : : :

hCLASP4 --KTKLQIIPGQLNITVECVPDLSNCITSSYVPLKPFE-KNCQNITVEVEEFVPEMTKY 567
hCLASP5 SLQRRVKSIPGLLRLEISTAPEIINCCLTPEMLPVKPPF-ENRTRPHKEILEFP--TREV 484
hCLASP3 SVLRRLRPITAQLKIDISPAPENPHYCLTPELLQVKLYP-DSRVRPTREILEFP--ARDV 553
hCLASP2 K-MAKLPVILGNLDITIDNVSSDFPNYVNSSYIPTKQFETCSKTPITFEVEEFVPCIPKH 560
hCLASP7 SLLRRLRPVTAQLKIDISPAPENPHFCLSPELLHIKPYP-DPRGRPTKEILEFP--AREV 540
hCLASP1 R-ISKMQTIPGSLDIAVDNVPLEHPNCVTSSFIPVKPFNMMAQTEPTVEVEEFVYDSTKY 658
: : : . * : : . . : : : : * : : * : * :

hCLASP4 CYPFTIYKNHLYVYPLQLKYDSQKTFAKARNIACVCEFRDSDSDASALKCIYGKPAGSV 627
hCLASP5 YVPHTVYRNLLYVYPQRLNFVN--KLASARNITIKIQFMCG-EDASNAMPVIFGKSSGPE 541
hCLASP3 YVPNTTYRNLLYIYPQSLNFAN--RQGSARNITVKVQFMYG-EDPSNAMPVIFGKSSCSE 610
hCLASP2 TQPYTIYTNHLYVYPKYLYDSQKSFAKARNIAICIEFKDSDEEDSQPLKCIYGRPGGPV 620
hCLASP7 YAPHTSYRNLLYVYPHSLNFSS--RQGSVRNLAVRVQYMTG-EDPSQALPVIIFGKSSCSE 597
hCLASP1 CRPYRVYKNQIYIYPKHLKYDSQKCFNKARNITVCIEFKNSDEESAKPLKCIYGKPEGPL 718
* * * : : * : : . . * : : : : : . * : : : : * : : .

hCLASP4 FTTNAYAVVSHHNQNPFEYDEIKIELPIHLHOKHHLLFTFYHVSCHINTKGTTKKQDTVE 687
hCLASP5 FLOQVYTAVTYHNKSPDFYEEVKIKLPAKLTVNHHLLFTFYHISCOQ-----KQASVE 595
hCLASP3 FSKRAYTAVVYHNRSDFHEEIKVKLPATLTDHLLFTFYHVSCQ-----KONTELE 664
hCLASP2 FTRSAFAAVLHHHQNPEFYDEIKIELPTQLHEKHHLLFTFYHVSCDNSSKGSTKKRDVE 680
hCLASP7 FTREAFTPVYVYHNKSPDFYEEFKLHLPACVTENHHLLFTFYHVSCOP-----RPGTALE 651
hCLASP1 FTSAYTAVLHHSQNPDFSDEVKIELPTQLHEKHHILFSFYHVTCHINAKANAKKKEALE 778
* . . : : * : : * : : * : : * : : : : : : : : : : : : : : : : : : : : :

hCLASP4 TPVGFAWVPLLKDGRITFEQQLPVSANLPPGYLNLNDAESRRQCNVDIKWVDGAKPLLK 747
hCLASP5 TLLGYSWLPILLNERLQTGSYCLPVALEKLPPNYSMHS AEKVPLQNPHIKWAEGHKGVFN 655
hCLASP3 TPVGTYWIPMLQNGRLKTGQFCLPVSLKPPQAYSVLSPEVP---LPGMKWVDNHKG VFN 721
hCLASP2 TQVGYSWLPPLLKDGRVVTSEQHIPVSANLPSGHLGYQELGMGRHYGPEIKWVDGGKPLLK 740
hCLASP7 TPVGFTWIPLLQHGRLRTGPFCLPVSDQPPPSYSVLTDPDA---LPGMRWVDG HKGVFS 708
hCLASP1 TSVGYAWLPLMKHDQIASQEYNIPIATSLPPNYLSFQDSASGKHGGSILKWVDGGKPLFK 838
* : : : : * : : . : : : : : : : : : : : : : : : : : : : : : : : : :

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FIG. 13  
2 of 6

|         |                                                              |     |
|---------|--------------------------------------------------------------|-----|
| hCLASP4 | FKSHLESTIYTQDLHVHKFFHHCQLIQS-----GSKEVPGELIKYLKCLHAM         | 794 |
| hCLASP5 | IEVQAVSSVHTQDNHLEKFFTLCHSLESQVTFPIRVLDQKISEMALEHELKLSIICLNSS | 715 |
| hCLASP3 | VEVVAVSSIHTQDPYLDKFFALVNALDEH-LFPVRIGDMRIMENNLENELKSSISALNSS | 780 |
| hCLASP2 | ISTHLVSTVYTQDQHLHNFFQYQCKTES-----GAQALGNELVKYLSLHAM          | 787 |
| hCLASP7 | VELTAVSSVHPQDPYLDKFFTLVHVLEEG-AFPFRLKDTVLSEGNVEQELRASLAALRLA | 767 |
| hCLASP1 | VSTFVVSTVNTQDPHVNAFFQECQKREKD-----MSQSPTS NFIR SCKNLLNVE     | 887 |

.. \*:: \*\* ::. \*\* : : .

|         |                                                                |     |
|---------|----------------------------------------------------------------|-----|
| hCLASP4 | EIQVMIQFLPVILMQLEF-----VLTNMTH-----EDDVP                       | 824 |
| hCLASP5 | RLEPLVLFHLVLDKLFQLSVQPMVIAGQTANFSQFASFESVVAIANSNLHNSKDLSKDQHG  | 775 |
| hCLASP3 | QLEPVVRFLHLLLDKLLLVIRPPVIAGQIVNLGQASFEAMASIINRLHKNLEGNHHDQHG   | 840 |
| hCLASP2 | EGHVMIAFLPTILNQLEF-----VLT-RAT-----QEEVA                       | 816 |
| hCLASP7 | SPEPLVAFSHHVLDKLVRLVIRPPIISGQIVNLGRGA FEAMAHVVS LVHRSLEAAQDARG | 827 |
| hCLASP1 | KIHAIMSFLPIILNQLEF-----VLVQNE-----EDEIT                        | 916 |

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|         |                                                               |     |
|---------|---------------------------------------------------------------|-----|
| hCLASP4 | INCTMV-LLHIVSKCHEEGLDS-----YLRSEFIKYS-----FRPEKP              | 860 |
| hCLASP5 | RNCLLASVHYVFRLEPEVQRDPKSGAPTALLDPRS YHTYGR TSAAAVSSKLLQARVMSS | 835 |
| hCLASP3 | RNSLLASYIHVFRLEPNTYPNSSSPG-PGGLGGSVHYATMARS AVR PASLNLNRSRSLN | 899 |
| hCLASP2 | VNVTRV- I IHVVAQCHEEGLES-----HLRSYVKYA-----YKAEPY             | 852 |
| hCLASP7 | HCPQLAAYVHYAFRLPGTEPSLPDGAPP-----VTVQAATLARGSGRPASLYLARSKSIS  | 883 |
| hCLASP1 | TTVTRV-LPDIVAKCHEEQLDH-----SVQSYIKFV-----FKTRAC               | 952 |

. . . :

|         |                                                             |     |
|---------|-------------------------------------------------------------|-----|
| hCLASP4 | SAPQAQLIH-----ETLATTMIAILKQS-----                           | 883 |
| hCLASP5 | SNPDLAGTHSAADEEVKNIMSSKIADRNC SRMSYYCSGSSDAPSSPA-----       | 882 |
| hCLASP3 | SNPDISGTPSPDDEVRSIIGSKGLDRSNSWVNTGGPKAAPWGSNPSPSAESTQAMDRSC | 959 |
| hCLASP2 | VASEYKTVH-----EELTKSMTTILKPS-----                           | 875 |
| hCLASP7 | SNPDLAVAPGSVDDEVSRILASKLLHEELA-LQ-----                      | 915 |
| hCLASP1 | KE---RPVH-----EDLAKNVTGLLKSN-----                           | 972 |

: . .

|         |                                                                  |      |
|---------|------------------------------------------------------------------|------|
| hCLASP4 | -----ADFLSINKLLKYS-----WFFFEIIAKSM                               | 907  |
| hCLASP5 | -----APRPASKKHFHEELALQ-----MUVSTGMVKSM                           | 910  |
| hCLASP3 | NRMSSHTETSSFLQTLTGRLP TKKLFHEELALQWVVC SGSVRESALQQA WFFFEI MVKSM | 1019 |
| hCLASP2 | -----ADFLT SNKLLRYS-----WFFFDVLIKSM                              | 899  |
| hCLASP7 | -----WVVS SAVREAILQHA-----WFFFQLMVKSM                            | 942  |
| hCLASP1 | -----DSPTVKHVLKHS-----WFFFAIILKSM                                | 995  |

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#### Cadherin Cleavage

|         |                                                               |      |
|---------|---------------------------------------------------------------|------|
| hCLASP4 | ATYLLLEENKIKLRFGRFPETYHHVLHSLLLAIIPHVTIRYAEIPDE---SRNVNYSLAS  | 964  |
| hCLASP5 | AQHVNMDKRDSEHRTFRSDFMDDITTIVNVVTSEIAALLVKPQKENEQA EKMNISLAF   | 970  |
| hCLASP3 | VHHLYFNDKLEAHRKSRFPERFMDDIAALVSTIASDIVSRFOKDTEM---VERLNTSLAF  | 1076 |
| hCLASP2 | AQHLENSKVKLIRNQRF PASYHHAETVVMMLMPHITQKFGDNPEA---SKNANHSLAV   | 956  |
| hCLASP7 | ALHLLLGQRDLTERKLRFPGRFLDDITALVGSVGLVITRVHKDVEL---AEHLNASLAF   | 999  |
| hCLASP1 | AQHLIDTNKIQLHRPQRFPE SYQNELDNLMVLS DHVIWKYKDALEE---TRRATHSVAR | 1052 |

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|         |                                                                     |      |
|---------|---------------------------------------------------------------------|------|
| hCLASP4 | FLKRCCLTMDRGFIENLINDYISGFSPKDP-----KVLA EYKFEFLQ TICNHEHYIPLNL      | 1019 |
| hCLASP5 | FLYDLLSLMDRGFVENLIRHYCSQLSAKLSNL---ETLISMRLEFLRILCSHEHYLNLNL        | 1027 |
| hCLASP3 | FLNDLLSVMDRGFVESLIKSCYQVSSKLYSLPNPSVLVSLRLD FLRIICSHEHYVTNLNL       | 1136 |
| hCLASP2 | FIKRCFTFMDRGFVEKQINNYISCFAPGDP-----KTLFEYKFEFLRVVCNHEHYIPLNL        | 1011 |
| hCLASP7 | FLSDLLSLVDRGFVESLVRAHYQVATRLQSSPNPAALLTLRMEFTRILCSHEHYVTNLNL        | 1059 |
| hCLASP1 | FLKRCFTFMDRGCFVEMVNYYISMFS S GDL-----KTL CQYKFD FLQEV CQHEHF I PLCL | 1107 |

\*: : : : \* \* . : . . . . . \* : : : \* : \* : \* : \* : \*

FIG. 13  
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Cadherin EC motif

hCLASP4 PMAFAKPKLQR-----VQDS--NLEYSLSDEYCKHHFLVGI LLRETSI 1060  
hCLASP5 FFMNADTAPTSP--CPSISSQNSSSSCSFQDQKIASMFDLTSEYRQQHFLTGI LFTELAA 1085  
hCLASP3 PCSLLTPPASPSVSSATSQSSGFSTNVQDQKIANMFELSVFPFQQHYLAGI VLTELAV 1196  
hCLASP2 PMPFGKGRIQR-----YQDL--QLDYSLTDEFCRNHFLVGI LLREVGT 1052  
hCLASP7 PCCPLSPPASPSVSSSTTSQSSTFSSQAPDPKVTSMFELSGPFQQHFLAGI LLTELAL 1119  
hCLASP1 PIRSANIPDLTP-----SES---TQELHASDMPEYSVTNEFCRKHFLIGI LLREVGF 1157  
. . . . . : : : : : \* \* \* : : .

hCLASP4 ALQDN----YFIRYTAISVIKLLIKHAFDTRYQHKNQQAIAQLYLPFVGLLENIQRL 1116  
hCLASP5 ALDAEGEGISKVQRKAVSAIHSLSSHLDPRCVKPEVKVKIAALYLPLVGI ILDALP-- 1143  
hCLASP3 ILDPDAEGLFGLHKKVINMVHNLSSHSDPRYSDPQIKARVAMLYLPLIGI IMETV-- 1254  
hCLASP2 ALQEFR----EVRLIAISVLKNLLIKHSFDDRYASRSHQARIATLYLPLFGLLIENVQRI 1108  
hCLASP7 ALEPEAEGAFILHKKAISAVHSLLCGHDTDPRYAEATVKARVAELYLPLLSIARDTLP-- 1177  
hCLASP1 ALQEDQ----DVRHLALAVLKNLMAKHSFDDRYREPRKQAQIASLYMPLYGMLLDNMPRI 1213  
\* : : : : : \* \* \* : : \* \* \* : : : :

hCLASP4 AGRDTLYSCA-----AMPN-S----ASRDEFPCGFTSPANRGSLSLTDKDTAYGS 1160  
hCLASP5 -----QL-----CDFTVADTRRYRTSGSD----- 1162  
hCLASP3 -----QLY-----DFTETHNQRGRPICIAITDD-- 1276  
hCLASP2 NVRDVSFPFVNAGMTVKDESLALPA-VNPLVTPQKGSTLDNSLHKDLLGAISGIASPYTT 1167  
hCLASP7 -----RLH-----DFAEGPGQRSRLASMLDSLTE 1201  
hCLASP1 YLKDLYPFTVNTSNQGSRDDLSLSTNGGFQSQTAIKHANSVDTSFSKDVLSNIAAFSSIAIS 1273  
. . . . . : :

hCLASP4 FQ-NGHGIKREDSRGLIPEGATGFPDQGNLTGEN-----TRQSSTRSSVSQYNRLDQYE 1213  
hCLASP5 -----EEQEGAGAINQNVALAIAGNNFNLT-----SGIVLSSLPYKQYNMLNADT 1208  
hCLASP3 -----YESEGSMISQTVAMAIAGTSVPQLTR----PGSFLTSTSGRQHTTFSAES 1324  
hCLASP2 STPNINSVRNADSRGLISTDSGNSLPERNSEKSNSLQKQSSSTLGNSVVRCDKLDQSE 1227  
hCLASP7 -----GEGDIAGTINPSVAMAIAGGPLAPGSR----ASISQGPPTASRAGCALSAES 1249  
hCLASP1 -----TVNHADSRASLASLDSNPSTNEKSSEKTDNCEKIPRLALIGSTLRFDRLDQAE 1327  
. . . . . : :

hCLASP4 TRSLLMCYLYIVKMISEDTLLTYWNKVSPQELINILILEVCLFHFYRMGKRNIARVHDA 1273  
hCLASP5 TRNLMICFLWIMKNADQSLIRKWIADLPSTQLNRILDLLFICVLCFEYKGKQSSDKVSTQ 1268  
hCLASP3 SRSLICLLWVLKNADETVLQKWFTDLSVLQLNRLLDLLYLVCVSCFEYKGKVFERNLSL 1384  
hCLASP2 IKSLLMCFLYILKSMSDDALFTYWNKASTSELMDDFTISEVCLHQFYMGKRYIARNQEG 1287  
hCLASP7 SRTLLACVLWVLKNTPEALLQRWATDLTLPQLGRLLDLLYLCLAAFEYKGKKAFFERINSL 1309  
hCLASP1 TRSLLMCFHIMKTISYETLIAYWQRAPSPVEVSDFFSILDVCLQNFYLGKRNIIRKIAA 1387  
: : \* \* : : \* : : : : : : : \* \* \* : :

hCLASP4 WLSKHFGIDR-----KSQTMPALNRNSGVMQARLQHLSSLESS----- 1311  
hCLASP5 VLQKSRDVKAR-----LEEALLRGEARGEMMRRRAPGNDRFPGLNEN--- 1311  
hCLASP3 TFKKSKDMRAK-----LEEAILGSIGARQEMVRRSRGQLERSPSGSAFGSQ 1430  
hCLASP2 LGPIVHDRKS-----QTLPVSRNRTGMMHARLQQLGSLDNS----- 1323  
hCLASP7 TFKKSLDMKAR-----LEEAILGTIGARQEMVRRSRERSPFGNPEN---- 1350  
hCLASP1 AFKFVQSTQNNGTLKGSNPSCQTSGLLAQWMHSTSRHEGHKQHRSTLPIIRGKN----- 1442  
. . . . . : : :

hCLASP4 -----FTLNHSSTTTEADIFHQALLEGNTATEVSLTVLDTISFFITQCFKTQLL 1359  
hCLASP5 --LRWKKEQTHWRQANEKLDKTKAELDQEALISGNLATEAHLIILDMQENITQASS-ALD 1368  
hCLASP3 ENLRWRKDMTHWRQNTTEKLDKSRAEIEHEALIDGNLATEANLIILDTLEIVVQTVS-VTE 1489  
hCLASP2 -----LTFNHSYGHSDADVLHQSLLEANIATEVCLTALDTLSLFTLAFKNQLL 1371  
hCLASP7 --VRWRKSVTHWKQTSRDVDKTKDEMEHEALVEGNLATEASLVVLDLTLEIIVQTVM-LSE 1407  
hCLASP1 --ALSNPKLLQMLDNTMTSNSNEIDIVHVDTEANIATEGCLTILDVLSLFTQTHQRQLQ 1500  
. . . . . : : : : : \* \* \* \* \* : :

FIG. 13  
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hCLASP4 NNDGHNPLMKKVFDIHLAFLKNGQSEVSLKHVFASLRAFISKFPSAFFKGRVNMCAAFCY 1419  
hCLASP5 CKDS---LLGGVLRVLVNSLNCDSQSTTYLTHCFATLRALIAKFGDLLFEEVEQCFLCH 1425  
hCLASP3 SKES---ILGGVLKVLHSMACNQSAVYLQHCFAQALVSKFPELLFEEETEQCADLCL 1546  
hCLASP2 ADHGHNPLMKKVFDVYLCFLQKHQSETALKNVFTALRSLIYKFPSTFYEGRADMCALCY 1431  
hCLASP7 ARES---VLGAVLKVVLYSLGSAQSALFLQHGLATQALVSKFPELLFEEDTELADLCL 1464  
hCLASP1 QCDCQNSLMKRGFDTYMLFFQVQNQSATAALKHVFASLRLVCKFPSAFFQGPADLCGSFCY 1560  
. : : : \* \* : : : \* : : \* : : \*

hCLASP4 EVLKCCTSKISSTRNEASALLYLLMRNNFEYTKRKTFLRTHLQIIIVSSQLIADVALSGG 1479  
hCLASP5 QVLHHCSSSMDVTRSQCATLYLLMR--FSFGATSNFARVKMQVTMSLASLVGRAPDFNE 1483  
hCLASP3 RLLRHCS SIGTIRSHPSASLYLLMR--QNFEIGNNFARVKMQVMSLSSLVGTSQNFNE 1604  
hCLASP2 EILKCCNSKLSSIRTEASQLLYFLMRNNFDYTGKKSFVRTHLQVIIISVSQLIADVVGIGE 1491  
hCLASP7 RLLRHCGSRISTIRTHASASLYLLMR--QNFEIGHNFARVKMQVTMSLSSLVGTTQNFSE 1522  
hCLASP1 EVLKCCNHRSRSTQTEASALLYLFMRKNFEFNQKQSIVRSHLQLIKAVSSQLIADAG-IGG 1619  
.: \* : : : \* : : : : : \*

hCLASP4 SRFQESLFIINNANSRPMKATAFFPAEVKDLTKRIRTVLMATAQMKHEKDPPEMLIDLQ 1539  
hCLASP5 EHLRRSLRTILAYSEEDTAMQMPFPPTQVEELLCLNLSILYDTVKMREFQEDPEMLMDLM 1543  
hCLASP3 EFLRRSLKTLITYAEEDLELRETTFPDQVQDLVFNLMILSDTVKMKHEKQEDPEMLIDLQ 1664  
hCLASP2 TRFQQSLSIINNCANSRLIKHTSFSSDVKDLTKRIRTVLMATAQMKHEKDPPEMLVDLQ 1551  
hCLASP7 EHLRRSLKTLITYAEEDMGLRSTFAEQVQDLMFNLMILTDTVKMKHEKQEDPEMLIDLQ 1582  
hCLASP1 SRFQHS LAITNNFANGDKQMKNSNFPFAEVKDLTKRIRTVLMATAQMKHEKDPPEMLVDLQ 1679  
.: \* : : : \* : : : : : \*

transmembrane  
hCLASP4 YSLAKSYASTPELRKTWLDMAKIHVKNGLFSEAAMCYVHVAALVAEFLHRKK----- 1592  
hCLASP5 YRIAKSYQASPDRLTLWLQNMAGEKHTKKKQYTEAMCLVHAAALVAEYLSMLEDH----- 1598  
hCLASP3 YRIAKGYQTSPE-RLTWLQNMAGKHSERSNHAEEAQCLVHSAALVAEYLSMLEDH----- 1718  
hCLASP2 YSLAKSYASTPELRKTWLDMAKIHVKNGLLSEAAMCYVHVTALVAEYLTRKG----- 1604  
hCLASP7 YRIARGYQGS PDRLTLWLQNMAGKHAELGNHAEAAQCMVHAAALVAEYLLLEDQ----- 1637  
hCLASP1 YSLANSYASTPELRRTWLESMAKIHARNGLLSEAAMCYIHIAALIAEYLRKGYWKVEKI 1739  
\* : \* : : \* : : : : \* : : : : \*

hCLASP4 -----LFPNGCSAFKKITPNIDEEGAMKEDAGMMD----- 1622  
hCLASP5 -----SYLPVGSVSFQNISSNVLEESVVSSEDTLSPDEDGV 1633  
hCLASP3 -----KYLPGCVTFQNISSNVLEESAVSDDVSPDEEGI 1753  
hCLASP2 -----VFRQGCTAFRVITPNIDEEASMMEDVGMQD----- 1634  
hCLASP7 -----RHLPVGCVSFQNISSNVLEESAISDDILSPDEEGF 1672  
hCLASP1 CTASLLSEDTHPCDSNSLLTTPSGGSMFSGMWPFLSITPNIKEGAAKEDSGMHD----- 1795  
: \* : \* : : \* : : \*

ITAM  
hCLASP4 ---VHYSEEVLELLEQCVGLWKAERYEIISEISKLVPIYKRRFEKLTQVYRTLHG 1679  
hCLASP5 CAGQYFTESGLVGLLEQAAELFSTGGLYETVNEVYKLVPILEAHREFRKLTLTHSKLQR 1693  
hCLASP3 CSGKYFTESGLVGLLEQAAASFSMAGMYEAVNEVYKLVPIHEANRDAKKLSTIHGKLQE 1813  
hCLASP2 ---VHFNEVDLMELLEQCADGLWKAERYELIADIYKLIPIYKRR----- 1677  
hCLASP7 CSGKHFTLGLVGLLEQAGYFTMGGLYEAVNEVYKNLPILEAHRDYKKLAAVHGKLQE 1732  
hCLASP1 ---TPYNENILVEQLYMCGEFLWKSERVELIADVKNPIIAVFEKQDFKKLSDLYYDIHR 1852  
.: \* : : : \* : : : : \*

ITAM DOCK motif DOCK motif ITAM  
hCLASP4 AYTKILEVMHTKKRLLGTFFRVAFYQGQFFFEEDGKEYIYKEFKLTGLSEISRLVKIYG 1739  
hCLASP5 AFDSIVNKDH--KRMFGTYFRVGFFG-SKFGDLDEQEFYKEFAITKLPEISHRLEAFYG 1750  
hCLASP3 AFSKIVHQSTGWERMFGTYFRVGFGY-TKFGDLDEQEFYKEFAITKLAEISHRLEGEYG 1872  
hCLASP2 -----DFFEDGKEYIYKEFKLTPLSEISQRLLKIYS 1710  
hCLASP7 AFTKIMHQSSGWERVFGTYFRVGFGY-AHFGDLDEQEFYKEFSITKLAEISHRLEEFYT 1791  
hCLASP1 SYLKVAEVVNSEKRLFGRYRVAFYQGQFFFEEDGKEYIYKEFKLTGLSEISQRLLKIYA 1912  
\* : : : \* : : : \*

FIG. 13  
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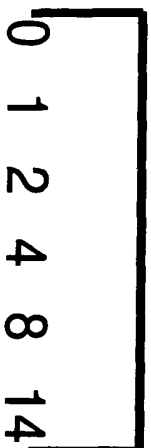




# Human CLASP-2 expression in T cells upon activation

**A)**

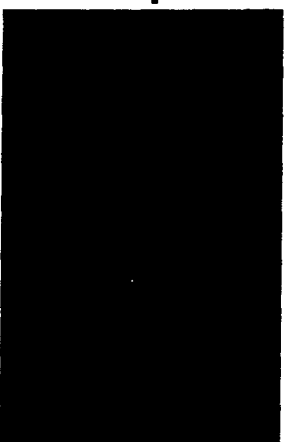
hours post  
activation



~ 7.5 kb -

CLASP-2

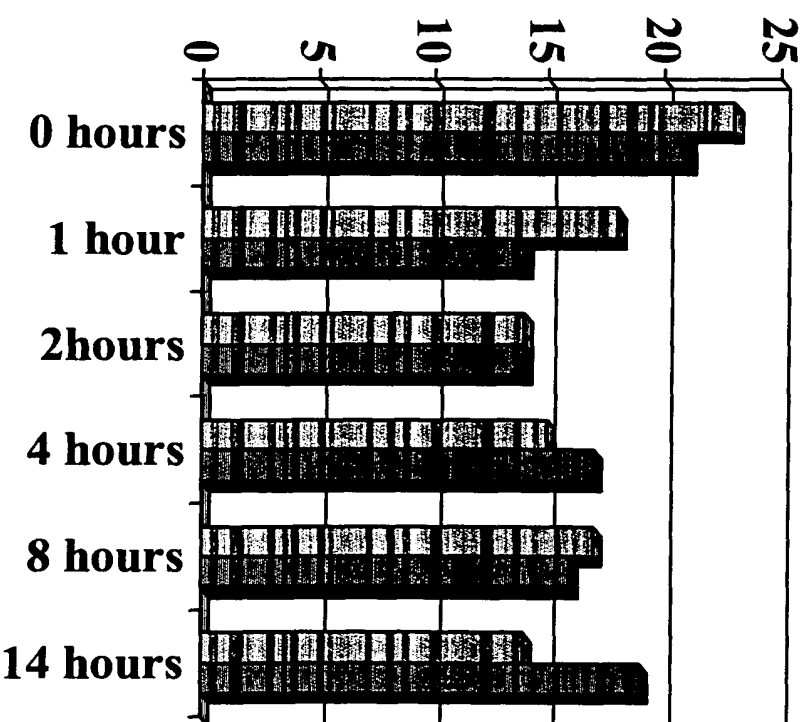
2.5 kb -



28s rRNA Ethbr. staining

**B)**

% of total  
signal



CLASP-2 (A)  
CLASP-2 (B)

hours post  
activation

09687837 " 101300